

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 16:17:47 ; Search time 17 Seconds
(without alignments)
759.612 Million cell updates/sec

Title: US-10-006-856A-194
Perfect score: 248
Sequence: 1 MGLSIFLLCVLGLSQAATP.....GVVYICKYVDWIRIMRNN 248

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	248	100.0	248	1	Q9UKR0 homo sapien
2	13	5.2	253	1	CPAD_HUMAN
3	13	5.2	394	1	UTRG_DESRO
4	13	5.2	431	1	URTB_DESRO
5	13	5.2	455	1	TMS5_MOUSE
6	13	5.2	457	1	TMS5_HUMAN
7	13	5.2	477	1	URT1_DESRO
8	13	5.2	477	1	URT2_DESRO
9	13	5.2	559	1	TPA_MOUSE
10	13	5.2	559	1	TPA_RAT
11	13	5.2	562	1	TPA_HUMAN
12	13	5.2	566	1	TPA_BOVIN
13	13	5.2	593	1	FA12_BOVIN
14	13	5.2	603	1	FA12_CAVPO
15	13	5.2	615	1	FA12_HUMAN
16	13	5.2	653	1	HGFA_MOUSE
17	13	5.2	811	1	TMS6_HUMAN
18	13	5.2	811	1	TMS6_MOUSE
19	12	4.8	244	1	KLK6_HUMAN
20	12	4.8	253	1	TRYB_DROER
21	12	4.8	253	1	TRYD_DROER
22	12	4.8	253	1	TRYD_DROME
23	12	4.8	253	1	TRYD_DROME
24	12	4.8	254	1	TRYP_SARBU
25	12	4.8	256	1	HYBP_HYPLI
26	12	4.8	256	1	TRYA_DROER
27	12	4.8	256	1	TRYA_DROME
28	12	4.8	256	1	TRYE_DROER
29	12	4.8	256	1	TRYE_DROME
30	12	4.8	258	1	TRYU_DROER
31	12	4.8	259	1	CFAD_FIG
32	12	4.8	262	1	TRYU_DROME
33	12	4.8	264	1	VDP_BOMMO

34	12	4.8	267	1	TRY7_ANOGA
35	12	4.8	274	1	TRY1_ANOGA
36	12	4.8	275	1	TRY3_ANOGA
37	12	4.8	275	1	TRY4_ANOGA
38	12	4.8	277	1	TRY2_ANOGA
39	12	4.8	281	1	TRYZ_DROER
40	12	4.8	418	1	HATT_HUMAN
41	12	4.8	422	1	DESI_HUMAN
42	11	4.4	235	1	TRYD_HUMAN
43	11	4.4	250	1	KLK9_HUMAN
44	11	4.4	250	1	KLKB_HUMAN
45	11	4.4	251	1	KLKE_HUMAN

ALIGNMENTS

RESULT 1
KLKC_HUMAN
ID KLKC_HUMAN STANDARD; PRT; 248 AA.
AC Q9UKR0; Q9UKR1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)
DE (KLK-15).
GN KLK12 OR KLK15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=201118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4."
RT Anticancer Res. 19:2843-2852(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;
RT "Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLK-15)."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBAJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."
RL Gene 257:119-130(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S., Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J., Danganan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S., Andreise T., Frankheim M., Attix C., Amico-Keller G., Cosfield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBAJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event:Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UKR0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UKR0-2; Sequence=VSP_005403;
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.

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CC      EMBL; AF135025; AAD26436.2; -
CC      EMBL; AF135025; AAR06065.1; -
CC      EMBL; AF243527; AAG33365.1; -
CC      EMBL; AC011473; AAG23258.1; -
CC      HSSP; P00763; 1DPO.
CC      MEROPS; S01.020; -
CC      Genew; HGNC:6360; KIK12.
CC      MIM; 605539; -
CC      GO; GO:000576; C:extracellular; NAS.
CC      GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
CC      GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
CC      InterPro; IPR009003; CysSer trypsin.
CC      InterPro; IPR001254; Peptidase S1.
CC      InterPro; IPR001314; Peptidase_S1A.
CC      Pfam; PF00089; trypsin; 1.
CC      PRINTS; PR00722; CHYMOTRYPSIN.
CC      SMART; SM00020; TRYPSIN; 1.
CC      PROSITE; PS00240; TRYPSIN_DOM; 1.
CC      PROSITE; PS00134; TRYPSIN_HIS; 1.
CC      PROSITE; PS00135; TRYPSIN_SER; 1.
CC      Hydrolase; Serine protease; Glycoprotein; Signal;
KW      Alternative splicing.
FT      SIGNAL          1   17
FT      CHAIN           18   248
FT      ACT_SITE        62   62
FT      ACT_SITE        108  108
FT      ACT_SITE        200  200
FT      DISULFID         28   161
FT      DISULFID         47   63
FT      DISULFID        133   235
FT      DISULFID        140   206
FT      DISULFID        172   186
FT      DISULFID        196   222
FT      CARBOHYD         24   24
FT      CARBOHYD        163   163
FT      VARSPPLIC       236   248
SQ      SEQUENCE        248 AA; 26733 MW; BB473E93F8BAF703 CRC64;
Query Match          100.0%; Score 248; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 7.9e-255;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  MGLSIFLLCVGLGSAATPKIFNGTTCGRNSOPWQVGLFGTSLRCGVLIDHRWYLTA 60
Db      1  MGLSIFLLCVGLGSAATPKIFNGTTCGRNSOPWQVGLFGTSLRCGVLIDHRWYLTA 60
QY      61  AHCSGSRYVRLGSHLSQLDWTETQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
Db      61  AHCSGSRYVRLGSHLSQLDWTETQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
QY      121  TSSVQPLPLPNDCAATAGTECHVSWGITNHPNRPFDLLQCLNLSIVSHATCHGVYPGRI 180
Db      121  TSSVQPLPLPNDCAATAGTECHVSWGITNHPNRPFDLLQCLNLSIVSHATCHGVYPGRI 180
QY      181  TSNMVCAGGVPGQDACQSDSGPLVCGVGLVQGLVSWGSGVPGCGDGIPIGVYTYICKYVDW 240
Db      181  TSNMVCAGGVPGQDACQSDSGPLVCGVGLVQGLVSWGSGVPGCGDGIPIGVYTYICKYVDW 240
QY      241  IRMIMRNN 248
Db      241  IRMIMRNN 248

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RESULT 2

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CFAD HUMAN
ID   CFAD_HUMAN          STANDARD;          PRT;   253 AA.
AC   P00746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Complement factor D precursor (EC 3.4.21.46) (C3 convertase activator)
DE   (Properdin factor D) (Adipsin).
DF   -
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 8-253 FROM N.A.
RX   MEDLINE=92250520; PubMed=1374388;
RA   White R.T., Damm D., Hancock N., Rosen B.S., Lowell B.B., Usher P.,
RA   Flier J.S., Spiegelman B.M.;
RT   "Human adipin is identical to complement factor D and is expressed
RT   at high levels in adipose tissue.";
RL   J. Biol. Chem. 267:9210-9213(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Flier J.S., Spiegelman B.M., Rosen B.M.;
RL   Patent number WO9006365, 14-JUN-1990.
RN   [3]
RP   SEQUENCE OF 26-252.
RX   MEDLINE=85000441; PubMed=6383466;
RA   Niemann M.A., Shown A.S., Bennett J.C., Volanakis J.E.;
RT   "Amino acid sequence of human D of the alternative complement
RT   pathway";
RL   Biochemistry 23:2482-2486(1984).
RN   [4]
RP   PARTIAL SEQUENCE OF 26-252.
RX   MEDLINE=84108950; PubMed=6363133;
RA   Johnson D.M.A., Gagnon J., Reid K.B.M.;
RT   "Amino acid sequence of human factor D of the complement system.
RT   Similarity in sequence between factor D and proteases of non-plasma
RT   origin.";
RL   FEBS Lett. 166:347-351(1984).
RN   [5]
RP   PARTIAL SEQUENCE OF 26-61 AND 194-220.
RX   MEDLINE=84256515; PubMed=6821372;
RA   Johnson D.M.A., Gagnon J., Reid K.B.M.;
RT   "Factor D of the alternative pathway of human complement.
RT   Purification, alignment and N-terminal amino acid sequences of the
RT   major cyanogen bromide fragments, and localization of the serine
RT   residue at the active site.";
RL   Biochem. J. 187:863-874(1980).
RN   [6]
RP   PARTIAL SEQUENCE OF 26-82.
RX   MEDLINE=80145719; PubMed=6987665;
RA   Volanakis J.E., Shown A.S., Bennett J.C., Mole J.E.;
RT   "Partial amino acid sequence of human factor D:homology with serine
RT   proteases";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:1116-1119(1980).
RN   [7]
RP   PARTIAL SEQUENCE OF 26-78.
RX   MEDLINE=81054886; PubMed=6776531;
RA   Davis A.E. III;
RT   "Active site amino acid sequence of human factor D.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:4938-4942(1980).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=94118317; PubMed=8289289;
RA   Narayana S.V.L., Carson M., El-Kabbani O., Kilpatrick J.M., Moore D.,
RA   Chen X., Bugg C.E., Volanakis J.E., Delucas L.J.;
RT   "Structure of human factor D. A complement system protein at 2.0-A
RT   resolution";
RL   J. Mol. Biol. 235:695-708(1994).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

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RX MEDLINE=96025834; PubMed=7592653;
 RA Kim S., Narayana S.V., Volanakis J.E.;
 FT "Crystal structure of a complement factor D mutant expressing
 RT enhanced catalytic activity.";
 RL J. Biol. Chem. 270:24399-24405(1995).
 CC -!- FUNCTION: Factor D cleaves factor B when the latter is complexed
 CC with factor C3b, activating the C3bb complex, which then becomes
 CC the C3 convertase of the alternate pathway. Its function is
 CC homologous to that of C1s in the classical pathway.
 CC -!- CATALYTIC ACTIVITY: Cleaves component factor B (Arg-Lys) when in
 CC complex with C3b or with cobra venom factor (CVF).
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- CAUTION: In addition to the conflicts shown in the feature table,
 CC Ref.3 sequence had a peptide in the wrong order and another one
 CC missing.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M84526; AAA35527.1; ALT_INIT.
 CC PIR; A40197; DEHU.
 CC PDB; 1DFP; 25-FEB-98.
 CC PDB; 1DST; 11-JUL-96.
 CC PDB; 1DSU; 17-AUG-96.
 CC PDB; 1BIO; 22-JUN-99.
 CC PDB; 1DIC; 22-JUL-99.
 CC PDB; 1FDP; 03-DEC-99.
 CC PDB; 1HFD; 22-JUN-99.
 CC MEROPS; S01.191; -.
 CC Genew; HGNC:2771; DF.
 CC MIN; J34350; -.
 CC GO; GO:0003817; F:complement factor D activity; TAS.
 CC GO; GO:0008236; F:serine-type peptidase activity; TAS.
 CC GO; GO:0006956; P:complement activation; TAS.
 CC GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00020; Tryp_SPC; 1.
 CC PROSITE; PS02040; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Complement alternate pathway; Plasma; Hydrolase; Serine protease;
 KW Zymogen; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 20
 FT PROPEP 21 25 POTENTIAL.
 FT CHAIN 26 253 ACTIVATION PEPTIDE (POTENTIAL).
 FT ACT_SITE 66 66 COMPLEMENT FACTOR D.
 FT ACT_SITE 112 112 CHARGE RELAY SYSTEM.
 FT ACT_SITE 208 208 CHARGE RELAY SYSTEM.
 FT DISULFID 51 67 CHARGE RELAY SYSTEM.
 FT DISULFID 148 214
 FT DISULFID 179 195
 FT DISULFID 204 229
 FT CONFLICT 26 26
 FT CONFLICT 35 35
 FT CONFLICT 40 40
 FT CONFLICT 49 49
 FT CONFLICT 52 52
 FT CONFLICT 59 59
 FT CONFLICT 63 63
 FT CONFLICT 73 73
 FT CONFLICT 83 86
 FT CONFLICT 83 84
 FT CONFLICT 94 95
 FT CONFLICT 96 96
 I -> M (IN REF. 1).
 H -> F (IN REF. 6).
 M -> V (IN REF. 6).
 H -> E (IN REF. 6).
 G -> A (IN REF. 1 AND 2).
 Q -> R (IN REF. 1 AND 2).
 S -> T (IN REF. 4).
 D -> G (IN REF. 4).
 HSLS -> THLP (IN REF. 3).
 HS -> ST (IN REF. 4).
 MISSING (IN REF. 4).
 D -> E (IN REF. 4).

FT CONFLICT 136 136
 FT CONFLICT 178 178
 FT CONFLICT 243 243
 FT CONFLICT 250 250
 FT CONFLICT 250 250
 FT STRAND 27 27
 FT TURN 28 28
 FT STRAND 30 30
 FT TURN 34 34
 FT TURN 38 38
 FT STRAND 40 40
 FT TURN 46 46
 FT STRAND 48 48
 FT TURN 58 58
 FT STRAND 60 60
 FT TURN 65 65
 FT HELIX 66 70
 FT STRAND 76 80
 FT STRAND 84 84
 FT TURN 90 91
 FT STRAND 93 102
 FT TURN 104 105
 FT TURN 112 113
 FT STRAND 116 120
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 FT STRAND 130 130
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 FT STRAND 147 152
 FT TURN 158 159
 FT STRAND 165 165
 FT STRAND 167 173
 FT HELIX 176 182
 FT TURN 183 184
 FT TURN 191 191
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 FT STRAND 202 202
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 FT TURN 208 209
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 FT STRAND 217 222
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 FT TURN 229 230
 FT STRAND 236 240
 FT HELIX 242 244
 FT STRAND 245 253
 SQ SEQUENCE 253 AA; 27004 MW; BD553B70BD55C6AD CRC64;
 Query Match 5.2%; Score 13; DB 1; Length 253;
 Best Local Similarity 100.0%; Pred. No. 6.8e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 198 GDSGGLVCGGVL 210
 DB 206 GDSGGLVCGGVL 218
 RESULT 3
 ID URTG DESRO STANDARD; PRT; 394 AA.
 AC P49150;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
 gamma).
 OS Desmodus rotundus (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
 OC Desmodontinae; Desmodus.

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OX NCBI_TaxID=9430;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA MEDLINE=92039036; PubMed=1937019;
RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
RA Alagon A., Donner P., Schleuning W.D.;
RT "The plasminogen activator family from the salivary gland of the
RT vampire bat Desmodus rotundus: cloning and expression.";
RL Gene 105:229-237(1991).
RN [2]
RP CHARACTERIZATION.
RA MEDLINE=93393059; PubMed=1309059;
RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
RA Donner P.;
RT "Plasminogen activators from the saliva of Desmodus rotundus (common
RT vampire bat): unique fibrin specificity.";
RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
CC -1- FUNCTION: Probably essential to support the feeding habits of this
CC exclusively haematophagous animal. Probable potent thrombolytic
CC agent.
CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC -----
CC EMBL; M63990; AAA31595.1; -.
CC PIR; JS0600; JS0600.
CC HSSP; P98119; IAS1.
CC MEROPS; S01.239; -.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Peptidase_S1.
CC Pfam; PF00051; kringle; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000395; Kringle; 1.
CC SMART; SM00130; KR; 1.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS00021; KRINGLE 1; 1.
CC PROSITE; PS50070; KRINGLE 2; 1.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; Signal; Multigene family.
FT SIGNAL 1 36 POTENTIAL.
FT CHAIN 37 394 SALIVARY PLASMINOGEN ACTIVATOR GAMMA.
FT DOMAIN 45 126 KRINGLE.
FT ACT_SITE 142 394 SERINE PROTEASE.
FT ACT_SITE 189 189 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 345 345 BY SIMILARITY.
FT DISULFID 45 126 BY SIMILARITY.
FT DISULFID 66 108 BY SIMILARITY.
FT DISULFID 97 121 BY SIMILARITY.
FT DISULFID 131 262 BY SIMILARITY.
FT DISULFID 174 190 BY SIMILARITY.
FT DISULFID 182 251 BY SIMILARITY.
FT DISULFID 276 351 BY SIMILARITY.
FT DISULFID 308 324 BY SIMILARITY.

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FT DISULFID 341 369 BY SIMILARITY.
FT CARBOHYD 315 315 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 394 AA; 44105 MW; 9CCD6F52FD81FCD CRC64;
Query Match 5.2%; Score 13; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 1e-05; 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;
QY 194 DACQGDSDGGPLVC 206
DB 339 DACQGDSDGGPLVC 351
RESULT 4
URTB_DESRO STANDARD; PRT; 431 AA.
AC P98121;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA
DE beta).
OS Desmodus rotundus (Vampire bat).
OC Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
OC Desmodontinae; Desmodus.
OX NCBI_TaxID=9430;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA MEDLINE=92039036; PubMed=1937019;
RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
RA Alagon A., Donner P., Schleuning W.D.;
RT "The plasminogen activator family from the salivary gland of the
RT vampire bat Desmodus rotundus: cloning and expression.";
RL Gene 105:229-237(1991).
RN [2]
RP CHARACTERIZATION.
RA MEDLINE=93393059; PubMed=1309059;
RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
RA Donner P.;
RT "Plasminogen activators from the saliva of Desmodus rotundus (common
RT vampire bat): unique fibrin specificity.";
RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
CC -1- FUNCTION: Probably essential to support the feeding habits of this
CC exclusively haematophagous animal. Probable potent thrombolytic
CC agent.
CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M63989; AAA31594.1; -.
CC PIR; JS0599; JS0599.
CC HSSP; P98119; IAS1.
CC MEROPS; S01.239; -.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.

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DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00051; kringie; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringie; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS90134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasmimogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringie; EGF-like domain; Signal; Multigene family.
 FT SIGNAL 1 36 POTENTIAL.
 FT CHAIN 37 431 SALIVARY PLASMINOGEN ACTIVATOR BETA.
 FT DOMAIN 37 75 EGF-LIKE.
 FT DOMAIN 82 163 KRINGLE.
 FT DOMAIN 179 431 SERINE PROTEASE.
 FT ACT_SITE 226 226 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 275 275 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 382 382 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 41 52 BY SIMILARITY.
 FT DISULFID 46 63 BY SIMILARITY.
 FT DISULFID 65 74 BY SIMILARITY.
 FT DISULFID 82 163 BY SIMILARITY.
 FT DISULFID 103 145 BY SIMILARITY.
 FT DISULFID 134 158 BY SIMILARITY.
 FT DISULFID 168 299 BY SIMILARITY.
 FT DISULFID 211 227 BY SIMILARITY.
 FT DISULFID 219 288 BY SIMILARITY.
 FT DISULFID 313 388 BY SIMILARITY.
 FT DISULFID 345 361 BY SIMILARITY.
 FT DISULFID 378 406 BY SIMILARITY.
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 431 AA; 48221 MW; 699B5B675B162CBF CRC64;
 Query Match 5.2%; Score 13; DB 1; Length 431;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 194 DACQDSGGPLVC 206
 Db 376 DACQDSGGPLVC 388
 RESULT 5
 TMS5 MOUSE
 ID TMS5 MOUSE STANDARD; PRT; 455 AA.
 AC Q9ER04; Q9ER02; Q9ER03;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).
 GN TMPSR5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Brain;
 RA Mitsui S.; Yamaguchi N.;
 RT "cDNA cloning of mouse spinesin.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Brain;
 RA Mitsui S.; Yamaguchi N.;
 RT "Molecular cloning of mouse type 4 spinesin.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=4;
 CC IsoId=Q9ER04-1; Sequence=Displayed;
 CC Name=1;
 CC IsoId=Q9ER04-2; Sequence=VSP_005397, VSP_005398;
 CC Name=2;
 CC IsoId=Q9ER04-3; Sequence=VSP_005395;
 CC Name=3;
 CC IsoId=Q9ER04-4; Sequence=VSP_005396;
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 1 SRCR domain.
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 or send an email to license@isb-sib.ch).
 CC EMBL; AB016229; BAR20276.1; -
 CC EMBL; AB016230; BAR20277.1; -
 CC EMBL; AB016423; BAR20278.1; -
 CC EMBL; AB041037; BAR40328.1; -
 CC HSP; P00763; IDPO.
 CC MEROPS; S01.313; -
 CC MGD; MGI:1933407; Impr55.
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR001254; Peptidase S1.
 CC InterPro; IPR001314; Peptidase S1A.
 CC InterPro; IPR001190; Srcr_receptor.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00020; Tryp_Spc; 1.
 CC PROSITE; PS50240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC PROSITE; PS00420; SRCR_1; FALSE_NEG.
 CC PROSITE; PS50287; SRCR_2; 1.
 KW Hydrolase; Serine protease; Transmembrane; Signal-anchor;
 KW Glycoprotein; Alternative splicing.
 FT DOMAIN 1 49 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 50 70 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 71 455 (POTENTIAL).
 FT DOMAIN 112 207 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 218 455 SRCR.
 FT ACT_SITE 258 258 SERINE PROTEASE.
 FT ACT_SITE 308 308 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 405 405 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT SITE 217 218 CLEAVAGE (POTENTIAL).
 FT DISULFID 135 196 BY SIMILARITY.
 FT DISULFID 148 206 BY SIMILARITY.
 FT DISULFID 209 328 BY SIMILARITY.
 FT DISULFID 243 259 BY SIMILARITY.
 FT DISULFID 374 390 BY SIMILARITY.
 FT DISULFID 401 429 BY SIMILARITY.
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 375 375 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 144 Missing (in isoform 2).
 FT VARSPLIC 1 10 /FtId=VSP_005395.
 FT VARSPLIC 1 10 Missing (in isoform 3).
 FT VARSPLIC 1 182 /FtId=VSP_005396.
 FT VARSPLIC 1 182 Missing (in isoform 1).
 FT VARSPLIC 1 182 /FtId=VSP_005397.

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FT VARSPLIC 183 192 GGLVEAWKP -> MEAQVGLLV (in isoform 1).
FT FTID=VSP 005398.
FT D -> G (IN REF. 1; BAB20277).
SQ SEQUENCE 455 AA; 49632 MW; 5CFC31789C6899AA CRC64;

Query Match
Best Local Similarity 5.2%; Score 13; DB 1; Length 455;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206
DB 399 DACQDSGGPLVC 411

RESULT 6
TMS5_HUMAN STANDARD; PRT; 457 AA.
AC Q9H3S3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).
GN TMPRSS5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX PubMed=11741986;
RA Yamaguchi N., Okui A., Yamada T., Nakazato H., Mitsui S.;
RT "Spinesin/TMPRSS5, a novel transmembrane serine protease, cloned from
human spinal cord.";
RL J. Biol. Chem. 277:6806-6812(2002).
CC -! SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -! TISSUE SPECIFICITY: Brain-specific. Predominantly expressed in
neurons, in their axons, and at the synapses of motoneurons in the
spinal cord.
CC -! SIMILARITY: Belongs to peptidase family S1.
CC -! SIMILARITY: Contains 1 SRCR domain.
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modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
CC
CC EMBL; AB028140; BAB20375.1; -.
CC HSSP; P00763; IDPO.
CC Genew; HGNC:14908; TMPRSS5.
CC
CC MIM; 606751.
CC
CC MEROPS; S01.313; -.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC InterPro; IPR001190; Srcr_receptor.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; TRYPSIN_DOM; 1.
CC DR PROSITE; PS50240; TRYPSIN_DOM; 1.
CC DR PROSITE; PS00134; TRYPSIN_HIS; 1.
CC DR PROSITE; PS00135; TRYPSIN_SER; 1.
CC DR PROSITE; PS00420; SRCR_1; FALSE_NEG.
CC DR PROSITE; PS50287; SRCR_2; FALSE_NEG.
KW Hydrolase; Serine protease; Transmembrane; Signal-anchor;
KW Glycoprotein.
FT DOMAIN 1 49 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 50 70 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 71 457 EXTRACELLULAR (POTENTIAL).

```

```

FT DOMAIN 112 207 SRCR
FT DOMAIN 218 457 SERINE PROTEASE.
FT ACT_SITE 258 308 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 308 308 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 405 405 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT SITE 217 218 CLEAVAGE (POTENTIAL).
FT SITE 217 218 BY SIMILARITY.
FT DISULFID 135 196 BY SIMILARITY.
FT DISULFID 148 206 BY SIMILARITY.
FT DISULFID 209 328 BY SIMILARITY.
FT DISULFID 243 259 BY SIMILARITY.
FT DISULFID 374 390 BY SIMILARITY.
FT DISULFID 401 429 BY SIMILARITY.
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 457 AA; 49574 MW; 64406AB4985A2651 CRC64;

Query Match
Best Local Similarity 5.2%; Score 13; DB 1; Length 457;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206
DB 399 DACQDSGGPLVC 411

RESULT 7
URT1_DESRO STANDARD; PRT; 477 AA.
AC P98A19;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Salivary plasminogen activator alpha 1 precursor (EC 3.4.21.68) (DSPA
alpha-1).
OS Desmodus rotundus (Vampire bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
OC Desmodontinae; Desmodus.
OX NCBI_TaxID=9430;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Salivary gland;
RX MEDLINE=92019036; PubMed=1937019;
RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
RT "The plasminogen activator family from the salivary gland of the
vampire bat Desmodus rotundus: cloning and expression.";
RL Gene 105:229-237(1991).
RN [2]
CHARACTERIZATION.
RX MEDLINE=93393059; PubMed=1309059;
RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
Donner P.;
RT "Plasminogen activators from the saliva of Desmodus rotundus (common
vampire bat): unique fibrin specificity.";
RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
RN [3]
X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RP TISSUE=Salivary gland;
RX MEDLINE=98022741; PubMed=9354616;
RA Renatus M., Stubbs M.T., Huber R., Bringmann P., Donner P.,
Schleuning W.D., Bode W.;
RT "Catalytic domain structure of vampire bat plasminogen activator: a
molecular paradigm for proteolysis without activation cleavage.";
RL Biochemistry 36:13483-13493(1997).
CC -! FUNCTION: Probably essential to support the feeding habits of this
exclusively haematophagous animal. Potent thrombolytic agent.
CC -! CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
plasminogen to form plasmin.

```

CC -!- ENZYME REGULATION: Activity toward plasminogen is stimulated in
 CC the presence of fibrin 1.
 CC -!- SUBUNIT: Monomer.
 CC -!- DOMAIN: The fibronectin type-I domain mediates binding to fibrin,
 CC and the kringle domain apparently mediates fibrin-induced
 CC stimulation of activity.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC -----
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 CC -----
 CC EMBL; M63987; AAA31591.1; -;
 CC EMBL; M63986; AAA31592.1; -;
 CC PIR; JS0597; JS0597.
 CC PDB; 1A5I; 23-MAR-99.
 CC MEROPS; S01.232; -;
 CC GlycoSuiteDB; P98119; -;
 CC InterPro; IPR003003; Cys Ser trypsin.
 CC InterPro; IPR006209; EGF_like.
 CC InterPro; IPR000083; Fibrinctn1.
 CC InterPro; IPR006210; IEGF.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR001254; Peptidase S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00008; EGF; 1.
 CC Pfam; PF00039; fn1; 1.
 CC Pfam; PF00051; kringle; 1.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC ProDom; PD000395; Kringle; 1.
 CC SMART; SM00181; EGF; 1.
 CC SMART; SM00058; FN1; 1.
 CC SMART; SM00130; KR; 1.
 CC SMART; SM00020; Tryp_SPC; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 1.
 CC PROSITE; PS50026; EGF_3; 1.
 CC PROSITE; PS01253; FIBRONECTIN_1; 1.
 CC PROSITE; PS00021; KRINGLE_1; 1.
 CC PROSITE; PS50070; KRINGLE_2; 1.
 CC PROSITE; PS50240; TRYPsin_DOM; 1.
 CC PROSITE; PS00134; TRYPsin_HIS; 1.
 CC PROSITE; PS00135; TRYPsin_SER; 1.
 CC Kring; EGF-like domain; Signal; Multigene family; 3D-structure.
 CC Kring; EGF-like domain; Signal; Multigene family; 3D-structure.
 CC SIGNAL 1 36
 CC CHAIN 37 477
 CC DOMAIN 40 82
 CC DOMAIN 83 121
 CC DOMAIN 128 209
 CC DOMAIN 225 477
 CC ACT_SITE 272 272
 CC ACT_SITE 321 321
 CC ACT_SITE 428 428
 CC DISULFID 42 72
 CC DISULFID 70 79
 CC DISULFID 87 98
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FT DISULFID 265 334
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 SQ SEQUENCE 477 AA; 53616 MW; AA06FD1739C10E5E CRC64;
 Query Match 5.2%; Score 13; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 194 DACQDSGGPLVC 206
 DB 422 DACQDSGGPLVC 434
 RESULT 8
 ID URT2 DESRO STANDARD; PRT; 477 AA.
 AC P15638;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Salivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA
 DE alpha-2) (BAT-PA) (T-plasminogen activator).
 OS Desmodus rotundus (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Chiroptera; Microchiroptera; Phyllostomidae;

Desmodontinae; Desmodus.
 NCBI_TaxID=9430;
 [1] SEQUENCE FROM N.A.
 TISSUE=Salivary gland;
 MEDLINE=92039036; PubMed=1937019;
 Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 Alagon A., Donner P., Schleuning W.D.,
 "The plasminogen activator family from the salivary gland of the
 vampire bat Desmodus rotundus: cloning and expression.";
 Gene 105:229-237(1991).
 [2]
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 TISSUE=Salivary gland;
 MEDLINE=90036667; PubMed=2509450;
 Gardell S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
 Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
 "Isolation, characterization, and cDNA cloning of a vampire bat
 salivary plasminogen activator.";
 J. Biol. Chem. 264:17947-17952(1989).
 [3]
 CHARACTERIZATION.
 MEDLINE=9339059; PubMed=1309059;
 Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
 Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 Donner P.;
 "Plasminogen activators from the saliva of Desmodus rotundus (common
 vampire bat): unique fibrin specificity.";
 Ann. N.Y. Acad. Sci. 667:395-403(1992).
 -!- FUNCTION: Probably essential to support the feeding habits of this
 exclusively haematophagous animal. Probable potent thrombolytic
 agent.
 -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 plasminogen to form plasmin.
 -!- ENZYME REGULATION: Activity toward plasminogen is stimulated in
 the presence of fibrin I.
 -!- SUBUNIT: Monomer.
 -!- DOMAIN: The fibronectin type-I domain mediates binding to fibrin,
 and the kringle domain apparently mediates fibrin-induced
 stimulation of activity
 -!- SIMILARITY: Belongs to peptidase family S1.
 -!- SIMILARITY: Contains 1 EGF-like domain.
 -!- SIMILARITY: Contains 1 fibronectin type I domain.
 -!- SIMILARITY: Contains 1 kringle domain.

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 or send an email to license@isb-sib.ch).

 EMBL; M63988; AAA31593.1; --
 EMBL; J05082; AAA31596.1; --
 FIR; A34369; A34369.
 FIR; J05098; J05098.
 HSSP; P98119; 1A51.
 MEROPS; S01.232; --
 InterPro; IPR009003; Cys Ser trypsin.
 InterPro; IPR006209; EGF_like.
 InterPro; IPR006083; Fibnctn1.
 InterPro; IPR006210; IEGF.
 InterPro; IPR000001; Kringle.
 InterPro; IPR001254; Peptidase_S1.
 InterPro; IPR001314; Peptidase_S1A.
 Pfam; PF00008; EGF; 1.
 Pfam; PF00039; fn1; 1.
 Pfam; PF00051; kringle; 1.
 Pfam; PF00089; trypsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 PRINTS; PR00018; KRINGLE.
 ProDom; PD000395; Kringle; 1.

DR SMART; SM00181; EGF; 1.
 DR SMART; SM00058; FN1; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; EGF-like domain; Signal; Multigene family.
 FT SIGNAL 1 36
 FT CHAIN 37 477
 FT DOMAIN 40 82
 FT DOMAIN 83 121
 FT DOMAIN 128 209
 FT DOMAIN 225 477
 FT ACT_SITE 272 272
 FT ACT_SITE 321 321
 FT ACT_SITE 428 428
 FT DISULFID 42 72
 FT DISULFID 70 79
 FT DISULFID 87 98
 FT DISULFID 92 109
 FT DISULFID 111 120
 FT DISULFID 128 209
 FT DISULFID 149 191
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 FT DISULFID 391 407
 FT DISULFID 424 452
 FT CARBOHYD 185 185
 FT CARBOHYD 398 398
 FT CONFLICT 403 403
 FT CONFLICT 417 417
 FT CONFLICT 435 435
 SQ SEQUENCE 477 AA; 53719 MW; 17486555C0E5077C CRC64;
 Query Match 5.2%; Score 13; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred.No. 1.2e-05; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 QY 194 DACQDSGGPLVC 206
 DB 422 DACQDSGGPLVC 434
 RESULT 9
 TPA MOUSE
 ID TPA_MOUSE STANDARD; PRT; 559 AA.
 AC P11214; Q91VP2;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (CPA)
 DE (t-PA) (t-plasminogen activator).
 GN PLAT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX SEQUENCE FROM N.A.
 RP MEDLINE=88087303; PubMed=2826484;
 RA Rickles R.J., Darrow A.L., Strickland S.;
 RT "Molecular cloning of complementary DNA to mouse tissue plasminogen

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
 DE (t-PA) (t-plasminogen activator) (Alteplase) (Reteplase).
 GN PLAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RX MEDLINE=83115262; PubMed=6337343;
 RA Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A.,
 RA Ward C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneker H.L.,
 RA Goeddel D.V., Collen D.;
 RT "Cloning and expression of human tissue-type plasminogen activator
 RT cDNA in E. coli.";
 RL Nature 301:214-221(1983).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Fetal lung;
 RX MEDLINE=88262579; PubMed=3133640;
 RA Sasaki H., Saito Y., Hayaashi M., Otsuka K., Niwa M.;
 RT "Nucleotide sequence of the tissue-type plasminogen activator cDNA
 RT from human fetal lung cells.";
 RL Nucleic Acids Res. 16:5695-5695(1988).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=88054470; PubMed=2824147;
 RA Reddy V.B., Garramone A.J., Sasak H., Wei C.-M., Watkins P., Galli J.,
 RA Haing N.;
 RT "Expression of human uterine tissue-type plasminogen activator in
 RT mouse cells using BPV vectors.";
 RL DNA 6:461-472(1987).
 RN [4]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86196143; PubMed=3009482;
 RA Frieznier Degen S.J., Rajput B., Reich E.;
 RT "The human tissue plasminogen activator gene.";
 RL J. Biol. Chem. 261:6972-6985(1986).
 RN [5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=84298137; PubMed=6089198;
 RA Ny T., Elgh F., Lund B.;
 RT "The structure of the human tissue-type plasminogen activator gene:
 RT correlation of intron and exon structures to functional and
 RT structural domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5355-5359(1984).
 RN [6]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86284200; PubMed=3090401;
 RA Harris T.J., Patel T., Marston F.A., Little S., Entage J.S.,
 RA Opendakker G., Volckaert G., Rombauts W., Billiau A., Somer P.;
 RT "Cloning of cDNA coding for human tissue-type plasminogen activator
 RT and its expression in Escherichia coli.";
 RL Mol. Biol. Med. 3:279-292(1986).
 RN [7]
 RN SEQUENCE FROM N.A. (ISOFORM SHORT).
 RC TISSUE=Umbilical vein;
 RX MEDLINE=90192129; PubMed=2107528;
 RA Siebert P.D., Fong K.;
 RT "Variant tissue-type plasminogen activator (PLAT) cDNA obtained from
 RT human endothelial cells.";
 RL Nucleic Acids Res. 18:1086-1086(1990).
 RN [8]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RN SEQUENCE OF 212-361 FROM N.A.
 RX MEDLINE=83169656; PubMed=6572897;
 RA Edlund T., Ny T., Raanby M., Heden L.-O., Palm G., Holmgren E.,
 RA Josephson S.;
 RT "Isolation of cDNA sequences coding for a part of human tissue
 RT plasminogen activator.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:349-352(1983).
 RN [10]
 RN SEQUENCE OF 1-36 FROM N.A.
 RX MEDLINE=85289338; PubMed=3161893;
 RA Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R.,
 RA Schleuning W.-D.;
 RT "Isolation and characterization of the human tissue-type plasminogen
 RT activator structural gene including its 5' flanking region.";
 RL J. Biol. Chem. 260:11223-11230(1985).
 RN [11]
 RN SEQUENCE OF 31-562 FROM N.A.
 RX MEDLINE=91291340; PubMed=1368681;
 RA Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
 RT "Purification and characterization of tissue plasminogen activator
 RT secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.";
 RL Agric. Biol. Chem. 55:1225-1232(1991).
 RN [12]
 RN SEQUENCE OF 36-562.
 RC TISSUE=Melanoma;
 RX MEDLINE=8500468; PubMed=6433976;
 RA Pohl G., Kaellstroem M., Bergsdorf N., Wallen P., Joernvall H.;
 RT "Tissue plasminogen activator: peptide analyses confirm an indirectly
 RT derived amino acid sequence, identify the active site serine residue,
 RT establish glycosylation sites, and localize variant differences.";
 RL Biochemistry 23:3701-3707(1984).
 RN [13]
 RN SEQUENCE OF 33-52 AND 311-330.
 RC TISSUE=Melanoma;
 RX MEDLINE=83209620; PubMed=6682760;
 RA Wallen P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H.;
 RT "Purification and characterization of a melanoma cell plasminogen
 RT activator.";
 RL Eur. J. Biochem. 132:681-686(1983).
 RN [14]
 RN STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=90092112; PubMed=2511186;
 RA Pfeiffer G., Schmidt M., Strube K.-H., Geyer R.;
 RT "Carbohydrate structure of recombinant human uterine tissue
 RT plasminogen activator expressed in mouse epithelial cells.";
 RL Eur. J. Biochem. 186:273-286(1989).
 RN [15]
 RN CARBOHYDRATE-LINKAGE SITE THR-96.
 RX MEDLINE=91159408; PubMed=1900431;
 RA Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.;
 RT "Tissue plasminogen activator has an O-linked fucose attached to
 RT threonine-61 in the epidermal growth factor domain.";
 RL Biochemistry 30:2311-2314(1991).
 RN [16]
 RN DISULFIDE BONDS IN KRINGLE 2.
 RX MEDLINE=91244765; PubMed=1645336;

RA Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.;
RT "Disulfide pairing of the recombinant kringle-2 domain of tissue
RL plasminogen activator produced in *Escherichia coli*.";
RJ J. Biol. Chem. 266:10070-10072(1991).
[17]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
RX MEDLINE=96200985; PubMed=9613982;
RA Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
RT "Two-chain human tissue-type plasminogen activator.";
RJ J. Mol. Biol. 258:117-135(1996).
[18]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN.
RX MEDLINE=9749126; PubMed=9305622;
RA Renatus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert U.,
RT "Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray
RJ crystal structure of single-chain human tPA.";
RL EMBO J. 16:4797-4805(1997).
[19]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
RX MEDLINE=92111803; PubMed=1310033;
RA de Vos A., Uitsch M.H., Kelley R.F., Padmanabhan K., Tulinski A.,
RT "Crystal structure of the kringle 2 domain of tissue plasminogen
RJ activator at 2.4-A resolution.";
RL Biochemistry 31:270-279(1992).
[20]
RP STRUCTURE BY NMR OF KRINGLE 2.
RX MEDLINE=90122799; PubMed=2558718;
RA Byeon I.-J.L., Kelley R.F., Llinas M.;
RT "Kringles-2 domain of the tissue-type plasminogen activator. 1H-NMR
RJ assignments and secondary structure.";
RL Eur. J. Biochem. 197:155-165(1991).
[22]
RP STRUCTURE BY NMR OF KRINGLE 2.
RX MEDLINE=92106329; PubMed=1762144;
RA Byeon I.-J.L., Llinas M.;
RT "Solution structure of the tissue-type plasminogen activator kringle
RJ 2 domain complexed to 6-aminohexanoic acid an antifibrinolytic
RT drug.";
RL J. Mol. Biol. 222:1035-1051(1991).
[23]
Query Match 5.2%; Score 13; DB 1; Length 562;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 194 DACQGDGGGLVC 206
Db 507 DACQGDGGGLVC 519
RESULT 12
TPA_BOVIN STANDARD; PRT; 566 AA.
AC Q28198;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
DE (t-PA) (t-plasminogen activator).
GN PLAT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ravn P., Berglund L., Petersen T.E.;
RT "Cloning and characterization of the bovine plasminogen activators uPA
RJ and tPA.";
RL Int. Dairy J. 5:605-617(1995).
CC -!- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen
CC to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By
CC controlling plasmin-mediated proteolysis, it plays an important
CC role in tissue remodeling and degradation, in cell migration and
CC many other physiopathological events.
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -!- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide
CC bond.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular.
CC -!- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
CC PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
CC ARG-314 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
CC -!- MISCELLANEOUS: Binds to the kringle structure of the fibrin A
CC chain. Binding to fibrin enhances its catalytic activity.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
CC -!- SIMILARITY: Contains 2 kringle domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X85800; CAA59795.1; -;
CC HSSP; P00750; 1RTF.
CC MEROPS; S01.232; -;
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR000083; Fibrinctn1.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Peptidase S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00008; EGF; 1.
CC Pfam; PF00039; fn1; 1.
CC Pfam; PF00051; kringle; 2.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000395; Kringle; 2.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00058; FN1; 1.
CC SMART; SM00130; FN1; 2.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS50026; EGF_3; 1.
CC PROSITE; PS01253; FIBRONECTIN_1; 1.
CC PROSITE; PS00021; KRINGLE_1; 1.
CC PROSITE; PS50070; KRINGLE_2; 2.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Plasma; Kringle; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 21
FT PROPEP 22 33 BY SIMILARITY.
FT CHAIN 34 566 TISSUE-TYPE PLASMINOGEN ACTIVATOR.

FT CHAIN 34 314 TISSUE-TYPE PLASMINOGEN ACTIVATOR A
 FT CHAIN 315 566 CHAIN.
 FT TISSUE-TYPE PLASMINOGEN ACTIVATOR B
 FT CHAIN.
 FT FIBRONECTIN TYPE-I.
 FT EGF-LIKE.
 FT KRINGLE 1.
 FT KRINGLE 2.
 FT SERINE PROTEASE.
 FT CHARGE RELAY SYSTEM.
 FT ACT_SITE 361 361 CHARGE RELAY SYSTEM.
 FT ACT_SITE 410 410 CHARGE RELAY SYSTEM.
 FT ACT_SITE 517 517 CHARGE RELAY SYSTEM.
 FT DISULFID 42 72 BY SIMILARITY.
 FT DISULFID 70 79 BY SIMILARITY.
 FT DISULFID 87 98 BY SIMILARITY.
 FT DISULFID 92 109 BY SIMILARITY.
 FT DISULFID 111 120 BY SIMILARITY.
 FT DISULFID 128 209 BY SIMILARITY.
 FT DISULFID 149 191 BY SIMILARITY.
 FT DISULFID 180 204 BY SIMILARITY.
 FT DISULFID 219 300 BY SIMILARITY.
 FT DISULFID 240 282 BY SIMILARITY.
 FT DISULFID 271 295 BY SIMILARITY.
 FT DISULFID 303 434 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 346 362 BY SIMILARITY.
 FT DISULFID 354 423 BY SIMILARITY.
 FT DISULFID 448 523 BY SIMILARITY.
 FT DISULFID 480 496 BY SIMILARITY.
 FT DISULFID 513 541 BY SIMILARITY.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 487 487 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 566 AA; 63701 MW; 286BBB4E32276C3 CRC64;

Query Match 5.2%; Score 13; DB 1; Length 566;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDGGPLVC 206
 Db 511 DACQDGGPLVC 523
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RESULT 13
 ID FA12 BOVIN STANDARD; PRT; 593 AA.
 AC P98140;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
 DE (HAP) (fragment).
 GN F12.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID:9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94242782; PubMed=8186251;
 RA Shibuya Y., Samba U., Okabe H., Kambara T., Yamamoto T.;
 RT "Primary structure of bovine Hageman factor (blood coagulation factor XII): comparison with human and guinea pig molecules.";
 RL Biochim. Biophys. Acta 1206:63-70(1994).
 RN [2]
 RP SEQUENCE OF 10-21; 350-364 AND 525-550.
 RX MEDLINE=77182112; PubMed=861210;
 RA Fujikawa K., Walsh A.K., Davie W.E.;
 RT "Isolation and characterization of bovine factor XII (Hageman factor).";
 RL Biochemistry 16:2270-2278(1977).
 CC -!- FUNCTION: Factor XII is a serum glycoprotein that participates in

the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin.
 -!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-ile bonds in factor VII to form factor VIIa and factor XI to form factor Xia.
 -!- PTM: O- AND N-GLYCOSYLATED (BY SIMILARITY).
 -!- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a complex bound to an anionic surface. Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to alpha-factor XIIIa and then to beta-factor XIIIa. Alpha-factor XIIIa activates factor XI to factor Xia. Bovine factor XII is cleaved only to alpha-factor XIIIa as it lacks the trypsin/kallikrein cleavage site.
 -!- SIMILARITY: Belongs to peptidase family S1.
 -!- SIMILARITY: Contains 2 EGF-like domains.
 -!- SIMILARITY: Contains 1 fibronectin type I domain.
 -!- SIMILARITY: Contains 1 fibronectin type II domain.
 -!- SIMILARITY: Contains 1 kringle domain.

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 EMBL; S70164; AAB30804.2; --
 PIR; S45281; S45281.
 HSSP; P00763; 1DPO.
 MEROPS; S01.211; --
 InterPro; IPR009003; Cys Ser trypsin.
 InterPro; IPR006209; EGF_like.
 InterPro; IPR000083; Fibrinctn.
 InterPro; IPR000562; FN_Type_II.
 InterPro; IPR006210; IEGF.
 InterPro; IPR000001; Kringle.
 InterPro; IPR001254; Peptidase_S1.
 InterPro; IPR001314; Peptidase_S1A.
 Pfam; PF00008; EGF; 2.
 Pfam; PF00039; fn1; 1.
 Pfam; PF00040; fn2; 1.
 Pfam; PF00051; kringle; 1.
 Pfam; PF00089; trypsin; 1.
 PRINTS; PS00722; CHYMOTRYPSIN.
 PRINTS; PR00013; FNYPEII.
 PRINTS; PR00018; KRINGLE.
 ProDom; PD000995; FN_Type_II; 1.
 ProDom; PD000395; Kringle; 1.
 SMART; SM00181; EGF; 2.
 SMART; SM00058; FN1; 1.
 SMART; SM00059; FN2; 1.
 SMART; SM00130; KR; 1.
 SMART; SM00020; Tryp_Spc; 1.
 SMART; SM00022; EGF_1; 2.
 PROSITE; PS01186; EGF_2; FALSE_NEG.
 PROSITE; PS00026; EGF_3; 2.
 PROSITE; PS01253; FIBRONECTIN_1; 1.
 PROSITE; PS00023; FIBRONECTIN_2; 1.
 PROSITE; PS00021; KRINGLE_1; 1.
 PROSITE; PS00070; KRINGLE_2; 1.
 PROSITE; PS00240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
 KW Hydrolase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 9
 FT CHAIN 10 349 ALPHA-FACTOR XIII HEAVY CHAIN.
 FT CHAIN 350 593 ALPHA-FACTOR XIII LIGHT CHAIN.
 FT DOMAIN 37 78 FIBRONECTIN TYPE-II.
 FT DOMAIN 84 121 EGF-LIKE 1.
 FT DOMAIN 123 163 FIBRONECTIN TYPE-I.
 FT DOMAIN 164 200 EGF-LIKE 2.

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FT DOMAIN 207 287 KRINGLE.
FT DOMAIN 297 333 PRO-RICH.
FT DOMAIN 350 593 SERINE PROTEASE.
FT ACT SITE 389 389 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 438 438 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 541 541 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 88 100 BY SIMILARITY.
FT DISULFID 94 109 BY SIMILARITY.
FT DISULFID 111 120 BY SIMILARITY.
FT DISULFID 125 153 BY SIMILARITY.
FT DISULFID 151 160 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 173 188 BY SIMILARITY.
FT DISULFID 190 199 BY SIMILARITY.
FT DISULFID 207 287 BY SIMILARITY.
FT DISULFID 230 269 BY SIMILARITY.
FT DISULFID 258 282 BY SIMILARITY.
FT DISULFID 336 463 BY SIMILARITY.
FT DISULFID 374 390 BY SIMILARITY.
FT DISULFID 382 452 BY SIMILARITY.
FT DISULFID 413 416 BY SIMILARITY.
FT DISULFID 479 547 BY SIMILARITY.
FT DISULFID 510 526 BY SIMILARITY.
FT DISULFID 537 568 BY SIMILARITY.
FT CARBOHYD 99 99 O-LINKED (FUC) (BY SIMILARITY).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 593 AA; 65148 MW; 721592BA792BD61F CRC64;

Query Match 5.2%; Score 13; DB 1; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 194 DACQDSGGPLVC 206
Db 535 DACQDSGGPLVC 547
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|||||

RESULT 14
ID _FAL2_CAVPO STANDARD; PRT; 603 AA.
AC Q04962;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
DE (HAF) (Fragment).
GN F12.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-37; 318-332 AND 353-373.
RC TISSUE=Liver;
RX MEDLINE=93003367; PubMed=1390917;
RA Semba U., Yamamoto T., Kunisada T., Shibuya Y., Tanase S.,
RA Kambara U., Okabe H.;
RT "Primary structure of guinea-pig Hageman factor: sequence around the
RT cleavage site differs from the human molecule.";
RL Biochim. Biophys. Acta 1159:113-121(1992).
CC -1- FUNCTION: Factor XII is a serum glycoprotein that participates in
CC the initiation of blood coagulation, fibrinolysis, and the
CC generation of bradykinin and angiotensin.
CC -1- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor
CC VII to form factor VIIa and factor XI to form factor Xla.
CC -1- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a
CC complex bound to an anionic surface. Prekallikrein is cleaved by
CC factor XII to form kallikrein, which then cleaves factor XII first
CC to alpha-factor Xla and then to beta-factor Xla. Alpha-factor
CC Xla activates factor XI to factor Xla.
CC -1- SIMILARITY: Belongs to peptidase family S1.

-1- SIMILARITY: Contains 2 EGF-like domains.
-1- SIMILARITY: Contains 1 fibronectin type I domain.
-1- SIMILARITY: Contains 1 fibronectin type II domain.
-1- SIMILARITY: Contains 1 kringle domain.
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EMBL; X68615; CAA48600.1; --
PIR; S28941; S28941.
HSP; P00763; IDPO.
MEROPS; S01.211; --
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR00742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR000083; Fibrinctnl.
InterPro; IPR000562; FN Type_II.
InterPro; IPR006210; IREG.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00008; EGF; 2.
Pfam; PF00039; fn1; 1.
Pfam; PF00040; fn2; 1.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00013; FNTYPEII.
PRINTS; PR00018; KRINGLE.
ProDom; PD000995; FN Type_II; 1.
ProDom; PD000395; Kringle; 1.
SMART; SM00181; EGF; 2.
SMART; SM00058; FN1; 1.
SMART; SM00059; FN2; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_Src; 1.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS01253; FIBRONECTIN_1; 1.
PROSITE; PS00023; FIBRONECTIN_2; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Blood coagulation; Plasma; Kringle; Serine protease;
KW Glycoprotein; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 358 ALPHA-FACTOR XIIA HEAVY CHAIN.
FT CHAIN 359 603 ALPHA-FACTOR XIIA LIGHT CHAIN.
FT DOMAIN 46 87 FIBRONECTIN TYPE-II.
FT DOMAIN 93 130 EGF-LIKE 1.
FT DOMAIN 132 172 FIBRONECTIN TYPE-I.
FT DOMAIN 173 209 EGF-LIKE 2.
FT DOMAIN 216 294 KRINGLE.
FT DOMAIN 312 342 PRO-RICH.
FT DOMAIN 359 603 SERINE PROTEASE.
FT ACT SITE 398 398 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 447 447 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 551 551 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 97 109 BY SIMILARITY.
FT DISULFID 103 118 BY SIMILARITY.
FT DISULFID 120 129 BY SIMILARITY.
FT DISULFID 134 162 BY SIMILARITY.
FT DISULFID 160 169 BY SIMILARITY.

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FT DISULFID 177 188 BY SIMILARITY.
 FT DISULFID 182 197 BY SIMILARITY.
 FT DISULFID 199 208 BY SIMILARITY.
 FT DISULFID 216 294 BY SIMILARITY.
 FT DISULFID 237 276 BY SIMILARITY.
 FT DISULFID 265 289 BY SIMILARITY.
 FT DISULFID 345 472 BY SIMILARITY.
 FT DISULFID 383 399 BY SIMILARITY.
 FT DISULFID 391 461 BY SIMILARITY.
 FT DISULFID 422 425 BY SIMILARITY.
 FT DISULFID 488 557 BY SIMILARITY.
 FT DISULFID 520 536 BY SIMILARITY.
 FT DISULFID 547 578 BY SIMILARITY.
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 603 AA; 66795 MW; 48DC6B946FB9ED59 CRC64;

Query Match 5.2%; Score 13; DB 1; Length 603;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQGDGSGPLVC 206
 DB 545 DACQGDGSGPLVC 557
 |||||

RESULT 15
 FA12 HUMAN STANDARD; PRT; 615 AA.
 AC P00748; P78339.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor) (HAF).
 GN F12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88007593; PubMed=2888762;
 RA Cool D.E., McGillivray R.T.A.;
 RT "Characterization of the human blood coagulation factor XII gene. Introns/exon gene organization and analysis of the 5'-flanking region.";
 RT J. Biol. Chem. 262:13662-13673(1987).
 RL [2]
 RP SEQUENCE FROM N.A., AND VARIANTS ALA-207; ASP-545 AND HIS-605.
 RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldane S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 4-615 FROM N.A.
 RX MEDLINE=86176794; PubMed=3754331;
 RA Tripodi M., Citarella F., Guida S., Galeffi P., Pantoni A., Cortese R.;
 RT "cDNA sequence coding for human coagulation factor XII (Hageman).";
 RL Nucleic Acids Res. 14:3146-3146(1986).
 RN [4]
 RP SEQUENCE OF 14-615 FROM N.A.
 RX MEDLINE=86033830; PubMed=3877053;
 RA Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D., McGillivray R.T.A.;
 RT "Characterization of human blood coagulation factor XII cDNA. Prediction of the primary structure of factor XII and the tertiary structure of beta-factor XIIa.";
 RL J. Biol. Chem. 260:13666-13676(1985).
 RN [5]
 RP SEQUENCE OF 146-615 FROM N.A.
 RX MEDLINE=86216049; PubMed=3011063;

RA Que B.G., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor XII (Hageman factor).";
 RL Biochemistry 25:1525-1528(1986).
 RN [6]
 RP SEQUENCE OF 20-379.
 RX MEDLINE=85182674; PubMed=3886654;
 RA McMullen B.A., Fujikawa K.;
 RT "Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated Hageman factor).";
 RL J. Biol. Chem. 260:5328-5341(1985).
 RN [7]
 RP SEQUENCE OF 354-362 AND 373-615.
 RX MEDLINE=83291041; PubMed=6604055;
 RA Fujikawa K., McMullen B.A.;
 RT "Amino acid sequence of human beta-factor XIIa.";
 RL J. Biol. Chem. 258:10924-10933(1983).
 RN [8]
 RP SEQUENCE OF 561-615 FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96133302; PubMed=8528215;
 RA Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle B., Engel W.;
 RT "The novel acceptor splice site mutation 11396(G->A) in the factor XII gene causes a truncated transcript in cross-reacting material negative patients.";
 RL Hum. Mol. Genet. 4:1235-1237(1995).
 RN [9]
 RP CARBOHYDRATE-LINKAGE SITE THR-109.
 RX MEDLINE=92184750; PubMed=1544894;
 RA Harris R.J., Ling V.T., Spellman M.W.;
 RT "O-linked fucose is present in the first epidermal growth factor domain of factor XII but not protein C.";
 RL J. Biol. Chem. 267:5102-5107(1992).
 RN [10]
 RP VARIANT WASHINGTON D.C. SER-590.
 RX MEDLINE=90046788; PubMed=2510163;
 RA Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving B., Saito H.;
 RT "Coagulation factor XII (Hageman factor) Washington D.C.: inactive factor XIIa results from Cys-571->Ser substitution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).
 RN [11]
 RP VARIANT LOCARNO PRO-372.
 RX MEDLINE=94325559; PubMed=8049433;
 RA Hovinga J.K., Schaller J., Stricker H., Willemin W.A., Furlan M., Laemmle B.;
 RT "Coagulation factor XII Locarno: the functional defect is caused by the amino acid substitution Arg-353->Pro leading to loss of a kallikrein cleavage site.";
 RL Blood 84:1173-1181(1994).
 RN [12]
 RP VARIANT TENRI CYS-53.
 RX MEDLINE=99290785; PubMed=10361128;
 RA Kondo S., Tokunaga F., Kawano S., Oono Y., Kumagai S., Koide T.;
 RT "Factor XII Tenri, a novel cross-reacting material negative factor XII deficiency, occurs through a proteasome-mediated degradation.";
 RL Blood 93:4300-4308(1999).
 CC -1- FUNCTION: Factor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin.
 CC -1- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor VII to form factor VIIa and factor XI to form factor Xla.
 CC -1- PTM: O- AND N-GLYCOSYLATED.
 CC -1- DISEASE: Defects in F12 do not cause any clinical symptoms. The sole effect is that whole-blood clotting time is prolonged.
 CC -1- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a complex bound to an anionic surface. Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor XIIa activates factor XI to factor Xla.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -1- SIMILARITY: Contains 1 fibronectin type I domain.

CC CC -!- SIMILARITY: Contains 1 fibronectin type II domain.
CC CC -!- SIMILARITY: Contains 1 kringle domain.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M31315; AAA70225.1; -.
DR EMBL; AF538691; AAM97932.1; -.
DR EMBL; M11723; AAA51986.1; -.
DR EMBL; M17466; AAB59490.1; -.
DR EMBL; M17464; AAB59490.1; JOINED.
DR EMBL; M17465; AAB59490.1; JOINED.
DR EMBL; M13147; AAA70224.1; -.
DR EMBL; U71274; AAB51203.1; -.
DR PIR; A29411; KFHU12.
DR HSP; P00763; LDPO.
DR MEROPS; S01.211; -.
DR Genew; HGNC:3530; F12.
DR MM; 234000; -.
DR GO; GO:0003805; F: blood coagulation factor XI activity; TAS.
DR GO; GO:0003806; F: blood coagulation factor XII activity; TAS.
DR GO; GO:0008236; F: serine-type peptidase activity; TAS.
DR GO; GO:0007596; P: blood coagulation; TAS.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00039; fn1; 1.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000995; FN_Type_II; 1.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
KW Hydrolase; Fibrinolysis; Signal; EGF-like domain; Repeat; Zymogen;
KW Polymorphism; Disease mutation.
FT SIGNAL 1 19
FT CHAIN 20 372 ALPHA-FACTOR XIIIA HEAVY CHAIN.
FT CHAIN 373 615 ALPHA-FACTOR XIIIA LIGHT CHAIN.
FT CHAIN 354 362 BETA-FACTOR XIIIA PART 1.
FT CHAIN 373 615 BETA-FACTOR XIIIA PART 2.
FT DOMAIN 47 88 FIBRONECTIN TYPE-II.
FT DOMAIN 94 131 EGF-LIKE 1.
FT DOMAIN 133 173 FIBRONECTIN TYPE-I.
FT DOMAIN 174 210 EGF-LIKE 2.

FT DOMAIN 217 295 KRINGLE.
FT DOMAIN 236 349 PRO-RICH.
FT DOMAIN 373 615 SERINE PROTEASE.
FT CARBOHYD 109 109 O-LINKED (GLCNAC...).
FT CARBOHYD 249 249 N-LINKED (POTENTIAL).
FT CARBOHYD 299 299 O-LINKED (POTENTIAL).
FT CARBOHYD 305 305 O-LINKED (POTENTIAL).
FT CARBOHYD 308 308 O-LINKED (POTENTIAL).
FT CARBOHYD 328 328 O-LINKED (POTENTIAL).
FT CARBOHYD 329 329 O-LINKED (POTENTIAL).

Query Match 5.2%; Score 13; DB 1; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQSDSGGPLVC 206
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Db 557 DACQSDSGGPLVC 569
||| |||||

Search completed: June 15, 2004, 16:24:19
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 16:21:07 ; Search time 45 Seconds
(without alignments)
1738.856 Million cell updates/sec

Title: US-10-006-856A-194
Perfect score: 248
Sequence: 1 MGLSIFLLCVLGSLQAATP.....GVYTYICKYVDWIRIMERN 248

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	26.2	111	4 Q9UKR2	Q9UKR2 homo sapien
2	31	12.5	234	11 Q9CV76	Q9CV76 mus musculus
3	14	5.6	681	13 Q7ZT70	Q7ZT70 lampetra ja
4	13	5.2	200	11 Q924U6	Q924U6 mus musculus
5	13	5.2	235	4 Q8N4E0	Q8N4E0 homo sapien
6	13	5.2	242	11 Q80VS4	Q80VS4 mus musculus
7	13	5.2	243	4 Q86VJ5	Q86VJ5 homo sapien
8	13	5.2	246	11 Q88301	Q88301 mus musculus
9	13	5.2	247	13 Q9W7Q5	Q9W7Q5 paralichthy
10	13	5.2	250	11 Q8CGR5	Q8CGR5 mus musculus
11	13	5.2	251	11 Q54854	Q54854 rattus norv
12	13	5.2	253	4 Q8WZB4	Q8WZB4 homo sapien
13	13	5.2	253	11 Q91Y82	Q91Y82 mus musculus
14	13	5.2	267	6 Q9MZZ6	Q9MZZ6 macaca fasc
15	13	5.2	277	5 Q96899	Q96899 scolopendra
16	13	5.2	300	4 Q96EF3	Q96EF3 homo sapien

17	13	5.2	320	13 Q7TOX2	Q7TOX2 xenopus lae
18	13	5.2	371	11 Q8CJ16	Q8CJ16 rattus norv
19	13	5.2	389	13 Q9PVX7	Q9PVX7 xenopus lae
20	13	5.2	395	4 Q9BZW1	Q9BZW1 homo sapien
21	13	5.2	445	11 Q8CJ17	Q8CJ17 rattus norv
22	13	5.2	455	11 Q8CDR0	Q8CDR0 mus musculus
23	13	5.2	516	4 Q9BU99	Q9BU99 homo sapien
24	13	5.2	562	4 Q86YK8	Q86YK8 homo sapien
25	13	5.2	562	6 Q8SQ23	Q8SQ23 sus scrofa
26	13	5.2	564	6 Q8MKB1	Q8MKB1 oryctolagus
27	13	5.2	597	11 Q35727	Q35727 mus musculus
28	13	5.2	609	11 Q80YCS	Q80YCS mus musculus
29	13	5.2	615	4 Q81ZZ5	Q81ZZ5 homo sapien
30	13	5.2	616	6 Q97507	Q97507 sus scrofa
31	13	5.2	653	11 Q8VCS4	Q8VCS4 mus musculus
32	13	5.2	1524	13 Q91674	Q91674 xenopus lae
33	12	4.8	85	5 Q8MVL1	Q8MVL1 boltenia vi
34	12	4.8	155	5 Q9Y1K4	Q9Y1K4 anopheles g
35	12	4.8	187	5 Q45045	Q45045 scirpophaga
36	12	4.8	253	5 Q8SXZ4	Q8SXZ4 drosophila
37	12	4.8	253	5 Q8MKZ1	Q8MKZ1 drosophila
38	12	4.8	254	5 Q9XYI0	Q9XYI0 rhizopertha
39	12	4.8	254	5 Q76520	Q76520 stomoxys ca
40	12	4.8	255	3 Q9Y7A9	Q9Y7A9 metarhizium
41	12	4.8	256	5 Q25081	Q25081 hypoderma l
42	12	4.8	256	5 Q9XYV1	Q9XYV1 rhizopertha
43	12	4.8	256	5 Q18599	Q18599 drosophila
44	12	4.8	258	5 Q9W5U8	Q9W5U8 drosophila
45	12	4.8	260	5 Q9V6P6	Q9V6P6 drosophila

ALIGNMENTS

RESULT 1

ID	Q9UKR2	PRELIMINARY;	PRT;	111 AA.
AC	Q9UKR2;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Kallikrein-like protein 5-related protein 2.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yousef G.M., Luo L., Diamandis E.P.;			
RT	"Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4."			
RL	Anticancer Res. 79:2843-2852 (1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21121728; PubMed=10675891;			
RA	Diamandis E.P., Yousef G.M., Lou L.Y., Magklara A., Obiezu C.;			
RT	"The new kallikrein gene family: implications in carcinogenesis."			
RL	Trends Endocrinol Metab. 11:54-60 (2000).			
DR	EMBL; AF135025; AAF06066.1; -			
DR	HSSP; P00752; IHIA.			
DR	GO; GO:0008233; F:peptidase activity; IEA.			
DR	GO; GO:0004295; F:trypsin activity; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	GO; GO:0006508; P:trypsin activity; IEA.			
DR	InterPro; IPR009003; Cys Ser trypsin.			
DR	InterPro; IPR001254; Peptidase_S1.			
DR	InterPro; IPR00089; trypsin; 1.			
DR	Protein; PS00134; TRYPSIN_HIS; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.			
KW	Hydrolase; Protease; Serine protease.			
SQ	SEQUENCE 111 AA; 11984 MW; 3E8EAB4295635D8D CRC64;			

Query Match 26.2%; Score 65; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 26-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 60
 Db 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 60

QY 61 AHCSG 65
 Db 61 AHCSG 65

RESULT 2

ID Q9CV76 PRELIMINARY; PRT; 234 AA.
 AC Q9CV76;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 2310008B01RIK protein (Fragment).
 GN 2310008B01RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Abburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki K., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wuyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AK009217; BAB26143.1; -.
 DR HSP; P00763; IDPO.
 DR MEROPS; S01.020; -.
 DR MGD; MGI:1916761; 2310008B01RIK.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;

Query Match 12.5%; Score 31; DB 11; Length 234;
 Best Local Similarity 100.0%; Pred.No. 1.1e-23;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDGGGLVCGVQLQGLVSWGSGVPCGQ 224
 Db 180 DACQDGGGLVCGVQLQGLVSWGSGVPCGQ 210

RESULT 3

Q7ZT70
 ID Q7ZT70 PRELIMINARY; PRT; 681 AA.
 AC Q7ZT70;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mannose-binding lectin associated serine protease-1.
 GN MASP-1.
 OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lethenteron.
 OX NCBI_TaxID=94989;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22593355; PubMed=12707349;
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsusita A., Takahashi M.,
 RA Matsushita M., Fujita T.,
 RT "Origin of Mannose-Binding Lectin-Associated Serine Protease (MASP)-1
 and MASP-3 Involved in the Lectin Complement Pathway Traced Back to
 the Invertebrate, Amphioxus.";
 RT J. Immunol. 170:4701-4707(2003).
 RL EMBL; AB089265; BAC75884.1; -.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0016431; F:oxidoreductase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002086; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Aex_Hydroxyl_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00084; sushi; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Lectin; Protease.
 SQ SEQUENCE 681 AA; 75277 MW; 27386FALL17C1D437 CRC64;

Query Match 5.6%; Score 14; DB 13; Length 681;
 Best Local Similarity 100.0%; Pred.No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 QDACCQDGGGLV 205
 Db 622 QDACCQDGGGLV 635

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RESULT 4
Q924U6 PRELIMINARY; PRT; 200 AA.
AC Q924U6
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Serine protease-like 1.
GN 1700036D21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mateni H., Takahashi T.;
RT "Mus musculus mRNA for serine protease-like gene spliced variant-1.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB047758; BAB63919.1; -.
DR HSSP; P00761; IANL.
DR MEROPS; S01.106; -.
DR MGD; MGI:1920586; 1700036D21RIK.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 200 AA; 22135 MW; 972959E4686EF603 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206
DB 128 DACQDSGGPLVC 140

RESULT 5
Q8N4E0 PRELIMINARY; PRT; 235 AA.
AC Q8N4E0
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC034529; AAH34529.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.

RESULT 6
Q80VS4 PRELIMINARY; PRT; 242 AA.
AC Q80VS4
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to kallikrein 14 (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044756; AAH44756.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
FT NON TER 1
SQ SEQUENCE 242 AA; 26059 MW; A3F8A624DE481D36 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 CQDSGGPLVCGG 208
DB 191 CQDSGGPLVCGG 203

RESULT 7
Q86VJ5 PRELIMINARY; PRT; 243 AA.
AC Q86VJ5
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to D component of complement (Adipsin) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hypothetical protein; Hydrolase; Protease; Serine protease.
FT NON TER 1
SQ SEQUENCE 235 AA; 25110 MW; 9DEF67A48D5913F6 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GDSGGLVCGGVL 210
DB 188 GDSGGLVCGGVL 200

RESULT 6
Q80VS4 PRELIMINARY; PRT; 242 AA.
AC Q80VS4
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to kallikrein 14 (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044756; AAH44756.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
FT NON TER 1
SQ SEQUENCE 242 AA; 26059 MW; A3F8A624DE481D36 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 CQDSGGPLVCGG 208
DB 191 CQDSGGPLVCGG 203

RESULT 7
Q86VJ5 PRELIMINARY; PRT; 243 AA.
AC Q86VJ5
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to D component of complement (Adipsin) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Spleen;
RX  MEDLINE=22388257; PubMed=12477932;
RA  Strausberg R.L., Collins E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Feingold S.A., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
RA  Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Spleen;
RX  Strausberg R.;
RL  Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC051001; AAH51001.1; -.
DR  GO; GO:0004263; F:chymotrypsin activity; IEA.
DR  GO; GO:0004295; F:trypsin activity; IEA.
DR  GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR  InterPro; IPR009003; Cys_Ser_trypsin.
DR  InterPro; IPR001254; Peptidase_S1.
DR  Pfam; PF00089; trypsin; 1.
DR  PRINTS; PR00722; CHYMOTRYPSIN.
DR  SMART; SM00020; Tryp_SPC; 1.
DR  PROSITE; PS00240; TRYPSIN_DOM; 1.
DR  PROSITE; PS00134; TRYPSIN_HIS; 1.
DR  PROSITE; PS00135; TRYPSIN_SER; 1.
FT  NON TER 1
SQ  SEQUENCE 243 AA; 25809 MW; 67F02995119490BC CRC64;

Query Match 5.2%; Score 13; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GDSGGPLVCGGV 210
DB 196 GDSGGPLVCGGV 208

RESULT 8
O88301 ID O88301 PRELIMINARY; PRT; 246 AA.
AC O88301;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine protease (BSP).
GN PRS18 OR MBSP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Matsui H., Takahashi T.;
RT "Mouse serine protease preferentially expressed in brain."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

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RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/C; TISSUE=Skin;
RA  Meier N., Dear T.N., Boehm T.;
RT "A novel serine protease expressed in the hair follicle."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL;
RA  Matsui H., Takahashi T.;
RT "The sequences of mouse serine protease gene expressed in brain."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BSLONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB015206; BAA28895.1; -.
DR EMBL; Y18723; CAA7269.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.236; -.
DR MGD; MGI:1343166; Prrs18.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 246 AA; 27496 MW; E20C080087139B63 CRC64;

Query Match 5.2%; Score 13; DB 11; Length 246;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 CQDSGGPLVCGG 208
DB 193 CQDSGGPLVCGG 205

RESULT 9
Q9W7Q5 ID Q9W7Q5 PRELIMINARY; PRT; 247 AA.
AC Q9W7Q5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Trypsinogen 3.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Suzuki T., Srivastava A.S., Kurokawa T.;
RT "Japanese flounder mRNA for trypsinogen 3."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029752; BAA82364.2; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.124; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.

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DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 247 AA; 26948 MW; DC4B647179DD972 CRC64;

Query Match          5.2%; Score 13; DB 13; Length 247;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206
DB 194 DACQDSGGPLVC 206
|||||

RESULT 10
Q8CGR5 PRELIMINARY; PRT; 250 AA.
AC Q8CGR5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glandular kallikrein KIK14.
GN KIK14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987;
RA Olsson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus musculus.";
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY152433; AN78421.1; -.
DR MGD; MGI:2447564; KIK14.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 250 AA; 27016 MW; F62FEBF2290FEBE8 CRC64;

Query Match          5.2%; Score 13; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 CQDSDGGPLVCG 208
DB 199 CQDSDGGPLVCG 211
|||||

RESULT 11
O54854 PRELIMINARY; PRT; 251 AA.
ID O54854
AC O54854;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 251 AA; 28014 MW; E21967EF06CEBBF9 CRC64;

Query Match          5.2%; Score 13; DB 11; Length 251;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 CQDSDGGPLVCG 208
DB 200 CQDSDGGPLVCG 212
|||||

RESULT 12
Q8WZB4 PRELIMINARY; PRT; 253 AA.
AC Q8WZB4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adipin/complement factor D precursor (EC 3.4.21.46).
DR DF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ralle M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AJ313463; CAC48304.1; -.
DR HSP; P00761; IAN1.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0003817; F:complement factor D activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.

```

DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMO0020; TRYP_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1 8 POTENTIAL.
FT CHAIN 9 253 ADIPSIN/COMPLEMENT FACTOR D PRECURSOR.
SQ SEQUENCE 253 AA; 27033 MW; 78906C209DEEA362 CRC64;

Query Match 5.2%; Score 13; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GDSGGPLVCGVYL 210
Db 206 GDSGGPLVCGVYL 218
|||||

RESULT 13
ID Q91Y82 PRELIMINARY; PRT; 253 AA.
AC Q91Y82;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neurosin (Protease, serine, 18).
GN PRS18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mitsui S., Yamaguchi N.;
RT "cDNA cloning and characterization of mouse brain specific serine
protease, Neurosin.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB008928; BAB5605.1; -.
DR EMBL; BC031119; AAH31119.1; -.
DR HSSP; P00761; IAN1.
DR MEROPS; S01.236; -.
DR MGD; MGI:1343166; Prs18.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin.1
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 253 AA; 28329 MW; CSEF98C7BEF2FBC1 CRC64;

Query Match 5.2%; Score 13; DB 11; Length 253;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 CQSGGGLVCGG 208
Db 200 CQSGGGLVCGG 212
|||||

RESULT 14
Q9MZ26 PRELIMINARY; PRT; 267 AA.
ID Q9MZ26
AC Q9MZ26;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
libraries";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB046651; BAB03569.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.299; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin.1
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMO0020; TRYP_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hypothetical protein; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 267 AA; 29516 MW; 69ACD18A0137AFC7 CRC64;

Query Match 5.2%; Score 13; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQSGGGLVLC 206
Db 159 DACQSGGGLVLC 171
|||||

RESULT 15
ID Q96899 PRELIMINARY; PRT; 277 AA.
AC Q96899;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasminogen activator SPA.
OS Scolopendra subspinipes.
OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Scolopendra.
OX NCBI_TaxID=55038;
RN [1]
RP SEQUENCE FROM N.A.
RA Sohn Y.-D., You W.K., Kim K.Y., Chung K.H., Park D.-H.;
RT "Cloning of a cDNA for a novel plasminogen activator from a Korean
centipede Scolopendra";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; U79521; AAD00320.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.122; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.

Wed Jun 16 11:19:03 2004

DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 277 AA; 30172 MW; EC62F80C8CB246C CRC64;

Query Match 5.2%; Score 13; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206
|||
DB 212 DACQDSGGPLVC 224

Search completed: June 15, 2004, 16:25:17
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 16:21:37 ; Search time 21 Seconds
(without alignments)
1135.976 Million cell updates/sec

Title: US-10-006-856a-194
Perfect score: 248
Sequence: 1 MGLSIFLLLCVLGLSQAATP.....GVVYICKYVDIMRMNRN 248

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR.78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	5.2	246	1 DBHU	complement factor
2	13	5.2	394	2 JS0600	t-plasminogen acti
3	13	5.2	431	2 JS0599	t-plasminogen acti
4	13	5.2	477	1 A34369	t-plasminogen acti
5	13	5.2	477	2 JS0597	t-plasminogen acti
6	13	5.2	477	2 JS0598	t-plasminogen acti
7	13	5.2	559	1 A35029	t-plasminogen acti
8	13	5.2	559	1 A29941	t-plasminogen acti
9	13	5.2	562	1 S45281	coagulation factor
10	13	5.2	593	2 S28941	coagulation factor
11	13	5.2	603	2 JS0912	coagulation factor
12	13	5.2	615	1 KFHU12	polypeptide - Afri
13	13	5.2	1524	2 T30337	complement factor
14	12	4.8	191	2 S54115	trypsin-like prote
15	12	4.8	254	2 S65465	trypsin-like prote
16	12	4.8	256	1 TRFF	trypsin-like prote
17	12	4.8	264	2 S32794	trypsin (EC 3.4.21
18	12	4.8	267	2 S40006	serine proteinase
19	12	4.8	271	2 S43308	trypsin (EC 3.4.21
20	12	4.8	274	2 S35339	trypsin (EC 3.4.21
21	12	4.8	275	2 S40007	trypsin (EC 3.4.21
22	12	4.8	275	2 S40005	trypsin (EC 3.4.21
23	12	4.8	277	2 S35340	trypsin (EC 3.4.21
24	12	4.8	285	2 T35195	probable serine pr
25	11	4.4	126	2 A23473	chymotrypsin-like
26	11	4.4	225	2 S45356	probable serine pr
27	11	4.4	237	2 S55378	serine proteinase
28	11	4.4	237	2 S68702	trypsin (EC 3.4.2
29	11	4.4	260	2 I56559	neuropsin - mouse

30	11	4.4	264	2 I38136	chymotrypsin-like
31	11	4.4	266	2 JC4850	trypsin-like prote
32	11	4.4	270	2 S56160	mast cell trypsin
33	11	4.4	273	2 A47246	trypsin (EC 3.4.2
34	11	4.4	274	2 JC4171	trypsin (EC 3.4.2
35	11	4.4	275	2 A35863	trypsin (EC 3.4.2
36	11	4.4	275	2 B35863	trypsin (EC 3.4.2
37	11	4.4	275	2 A32410	trypsin (EC 3.4.2
38	11	4.4	275	2 C35863	mast cell protein
39	11	4.4	276	2 A38654	coagulation factor
40	11	4.4	309	2 B49878	coagulation factor
41	11	4.4	343	1 A57014	u-plasminogen acti
42	11	4.4	400	1 A48050	u-plasminogen acti
43	11	4.4	431	1 UKHU	u-plasminogen acti
44	11	4.4	433	1 UKBY	u-plasminogen acti
45	11	4.4	433	1 JN0560	u-plasminogen acti

ALIGNMENTS

RESULT 1

DBHU

complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
N;Alternate names: adipsin; C3 convertase activator
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 31-Dec-1992 #text_change 08-Dec-2000
C;Accession: A40197; A00936; A60571; S66645
R;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.; J. Biol. Chem. 267, 9210-9213, 1992
A;Title: Human adipsin is identical to complement factor D and is expressed at high l
A;Reference number: A40197; MUID:92250520; PMID:1374388
A;Accession: A40197
A;Molecule type: mRNA
A;Residues: 1-246 <WHI>
R;Cross-references: GB:M84526
R;Niemann, M.A.; Bhowm, A.S.; Bennett, J.C.; Volanakis, J.B.
Biochemistry 23, 2482-2486, 1984
A;Title: Amino acid sequence of human D of the alternative complement pathway.
A;Reference number: A00936; MUID:85000441; PMID:6383466
A;Accession: A00936

†

Result No.	Score	Query Match	Length	DB ID	Description
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1	13	5.2	246	1 DBHU	complement factor
2	13	5.2	394	2 JS0600	t-plasminogen acti
3	13	5.2	431	2 JS0599	t-plasminogen acti
4	13	5.2	477	1 A34369	t-plasminogen acti
5	13	5.2	477	2 JS0597	t-plasminogen acti
6	13	5.2	477	2 JS0598	t-plasminogen acti
7	13	5.2	559	1 A35029	t-plasminogen acti
8	13	5.2	559	1 A29941	t-plasminogen acti
9	13	5.2	562	1 S45281	coagulation factor
10	13	5.2	593	2 S28941	coagulation factor
11	13	5.2	603	2 JS0912	coagulation factor
12	13	5.2	615	1 KFHU12	polypeptide - Afri
13	13	5.2	1524	2 T30337	complement factor
14	12	4.8	191	2 S54115	trypsin-like prote
15	12	4.8	254	2 S65465	trypsin-like prote
16	12	4.8	256	1 TRFF	trypsin-like prote
17	12	4.8	264	2 S32794	trypsin (EC 3.4.21
18	12	4.8	267	2 S40006	serine proteinase
19	12	4.8	271	2 S43308	trypsin (EC 3.4.21
20	12	4.8	274	2 S35339	trypsin (EC 3.4.21
21	12	4.8	275	2 S40007	trypsin (EC 3.4.21
22	12	4.8	275	2 S40005	trypsin (EC 3.4.21
23	12	4.8	277	2 S35340	trypsin (EC 3.4.21
24	12	4.8	285	2 T35195	probable serine pr
25	11	4.4	126	2 A23473	chymotrypsin-like
26	11	4.4	225	2 S45356	probable serine pr
27	11	4.4	237	2 S55378	serine proteinase
28	11	4.4	237	2 S68702	trypsin (EC 3.4.2
29	11	4.4	260	2 I56559	neuropsin - mouse

Query Match

5.2†; Score 13; DB 1; Length 246;

A;Molecule type: protein
A;Residues: 19-44,'G',46-51,'Q',53-75,'TH',78,'P',80-83,'XXRTIE',90-172,86-91,185-23;
A;Note: a few residues were assigned from the previously published sequence of Reid et
R;Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.;
Mol. Immunol. 27, 637-644, 1990
A;Title: Molecular and functional identification and purification of complement compo
A;Reference number: A60571; MUID:90370044; PMID:2395435
A;Accession: A60571
A;Molecule type: protein
A;Residues: 19-20,'XX',23-27,'XX',30-31,'XX',34,'X',36-40 <MIY>
R;Balke, N.; Holtkamp, U.; Hoerl, W.H.; Teschesche, H.
FEBS Lett. 371, 300-302, 1995
A;Title: Inhibition of degradation of human polymorphonuclear leukocytes by complem
A;Reference number: S66645; MUID:96013156; PMID:7556615
A;Accession: S66645
A;Status: preliminary
A;Molecule type: protein
A;Residues: 19-44,'C',46-48 <BAL>
C;Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, acti
C;Genetics:
A;Gene: GDB:DF
A;Cross-references: GDB:132645; OMIM:134350
A;Map position: Xpter-Xqter
C;Superfamily: trypsin; trypsin homology
C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-246/Product: complement factor D {fragment} #status experimental <MAT>
F;19-241/Domain: trypsin homology <TRY>
F;44-60,141-207,172-189,197-222/Disulfide bonds: #status predicted
F;59,105,201/Active site: His, Asp, Ser #status predicted

Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GDSGGPLVCGVLC 210
|||||||
Db 199 GDSGGPLVCGVLC 211

RESULT 2

JS0600
t-plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat
N:Alternate names: tissue plasminogen activator
C:Species: Desmodus rotundus (common vampire bat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: JS0600
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991
A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A:Reference number: JS0597; MUID:92039036; PMID:1937019
A:Accession: JS0600
A:Molecule type: mRNA
A:Residues: 1-394 <KRA>
A:CROSS-references: GB:M63990; NID:g166076; PIDN:AAA31595.1; PID:g166079
A:Note: The authors translated the codon ATC for residue 75 as Thr
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-394/Product: plasminogen activator gamma #status predicted <PLA>
F:145-126/Domain: kringle homology <KRG>
F:143-388/Domain: trypsin homology <TRY>
F:145-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bonds:
F:189,239,345/Active site: His-Ser (plasmin) #status predicted
F:189,239,345/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:315/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 5.2%; Score 13; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSDGGPLVC 206
|||||||
Db 339 DACQDSDGGPLVC 351

RESULT 3

JS0599
t-plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat
N:Alternate names: tissue plasminogen activator
C:Species: Desmodus rotundus (common vampire bat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: JS0599
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991
A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A:Reference number: JS0597; MUID:92039036; PMID:1937019
A:Accession: JS0599
A:Molecule type: mRNA
A:Residues: 1-431 <KRA>
A:CROSS-references: GB:M63989; NID:g166076; PIDN:AAA31594.1; PID:g166077
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-431/Product: plasminogen activator beta #status predicted <PLA>
F:41-74/Domain: EGF homology <EGF>
F:82-163/Domain: kringle homology <KRG>
F:180-425/Domain: trypsin homology <TRY>
F:41-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide bond
F:139,352/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:179-180/Cleavage site: His-Ser (plasmin) #status predicted
F:226,275,382/Active site: His, Asp, Ser #status predicted
F:345-361,378-406/Disulfide bonds: #status predicted

Query Match 5.2%; Score 13; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSDGGPLVC 206
|||||||
Db 376 DACQDSDGGPLVC 388

RESULT 4

A34369
t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
C:Species: Megaderma lyra
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A34369
R:Gardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Ja
J. Biol. Chem. 264, 17947-17952, 1989
A:Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plas
A:Reference number: A34369; MUID:90036867; PMID:2509450
A:Accession: A34369
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-477 <GAR>
A:CROSS-references: GB:J05082; NID:g166080; PIDN:AAA31596.1; PID:g166081
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-477/Product: plasminogen activator #status predicted <PLA>
F:42-79/Domain: kringle homology <KRG>
F:87-120/Domain: EGF homology <EGF>
F:128-209/Domain: kringle homology <KRG>
F:226-471/Domain: trypsin homology <TRY>
F:426-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,35
F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 5.2%; Score 13; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSDGGPLVC 206
|||||||
Db 422 DACQDSDGGPLVC 434

RESULT 5

JS0597
t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor - common vampire bat
N:Alternate names: tissue plasminogen activator
C:Species: Desmodus rotundus (common vampire bat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: JS0597
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.;
Gene 105, 229-237, 1991
A:Title: The plasminogen activator family from the salivary gland of the vampire bat
A:Reference number: JS0597; MUID:92039036; PMID:1937019
A:Accession: JS0597
A:Molecule type: mRNA
A:Residues: 1-477 <KRA>
A:CROSS-references: GB:M63987; NID:g166070; PIDN:AAA31591.1; PID:g166071
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-477/Product: plasminogen activator alpha-1 #status predicted <PLA>
F:42-79/Domain: kringle homology <KRG>
F:87-120/Domain: EGF homology <EGF>
F:128-209/Domain: kringle homology <KRG>
F:226-471/Domain: trypsin homology <TRY>
F:426-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,35
F:153,398/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:225-226/Cleavage site: His-Ser (plasmin) #status predicted

F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 5.2%; Score 13; DB 2; Length 477;

Best Local Similarity 100.0%; Pred. No. 5.1e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSDSGPLVC 206

|||||

DB 422 DACQDSDSGPLVC 434

RESULT 6

JS0598

t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat

N:Alternate names: tissue plasminogen activator

C:Species: Desmodus rotundus (common vampire bat)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

C:Accession: JS0598

R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don

Gene 105, 229-237, 1991

A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des

A:Reference number: JS0597; MUID:92039036; PMID:1937019

A:Accession: JS0598

A:Molecule type: mRNA

A:Residues: 1-477 <KRA>

A:Cross-references: GB:M63988; NID:gl66074; PIDN:AAA1593.1; PID:gl66075

C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-36/Domain: propeptide #status predicted <PRO>

F:37-47/Domain: plasminogen activator alpha-2 #status predicted <PLA>

F:42-79/Domain: fibronectin type I repeat homology <IFR>

F:87-120/Domain: EGF homology <EGF>

F:128-209/Domain: trypsin homology <TRY>

F:226-471/Domain: kringle homology <KR>

F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4

F:185,398/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:225-226/Cleavage site: His-Ser (plasmin) #status predicted

F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 100.0%; Pred. No. 5.1e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSDSGPLVC 206

|||||

DB 422 DACQDSDSGPLVC 434

RESULT 7

A35029

t-plasminogen activator (EC 3.4.21.68) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A35029; A31597

R:Feng, P.; Ohlsson, M.; Ny, T.

J. Biol. Chem. 265, 2022-2027, 1990

A:Title: The structure of the TATA-less rat tissue-type plasminogen activator gene. Spec

A:Reference number: A35029; MUID:90130448; PMID:2105315

A:Accession: A35029

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-559 <FEN>

A:Cross-references: GB:M31197; NID:g207429; PIDN:AAA42261.1; PID:g207431; GB:J05226

R:NY, T.; Leonardson, G.; Haueh, A.J.W.

DNA 7, 671-677, 1988

A:Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activator

A:Reference number: A31597; MUID:89170114; PMID:3148445

A:Accession: A31597

A:Molecule type: mRNA

A:Residues: 1-379, 'K', 381-559 <NYT>

A:Cross-references: GB:M23697; NID:g530159; PIDN:AAA41812.1; PID:g530160

C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-29/Domain: propeptide #status predicted <PRO>
F:30-559/Domain: t-plasminogen activator #status predicted <MAT>
F:30-308/Domain: t-plasminogen activator chain A #status predicted <ACH>
F:38-75/Domain: fibronectin type I repeat homology <IFR>
F:83-116/Domain: EGF homology <EGF>
F:124-205/Domain: kringle homology <KRI>
F:213-294/Domain: kringle homology <KR2>
F:309-559/Domain: t-plasminogen activator chain B #status predicted <BCH>
F:309-553/Domain: trypsin homology <TRY>
F:38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,29
F:149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted
F:355,404,510/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 100.0%; Pred. No. 5.9e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSDSGPLVC 206

|||||

DB 504 DACQDSDSGPLVC 516

RESULT 8

A29941

t-plasminogen activator (EC 3.4.21.68) precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A29941; S48205; S48207; S48206

R:Richles, R.J.; Darrow, A.L.; Strickland, S.

J. Biol. Chem. 263, 1563-1569, 1988

A:Title: Molecular cloning of complementary DNA to mouse tissue plasminogen activator

A:Reference number: A29941; MUID:88087303; PMID:2826484

A:Accession: A29941

A:Molecule type: mRNA

A:Residues: 1-559 <PIC>

A:Cross-references: GB:J03520; NID:g202109; PIDN:AAA40470.1; PID:g202110

R:Liijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.

Eur. J. Biochem. 224, 863-871, 1994

A:Title: Characterization of the murine plasma fibrinolytic system.

A:Reference number: S48202; MUID:95010076; PMID:7523120

A:Accession: S48205

A:Molecule type: protein

A:Residues: 33-37, 'X', 39-40 <LIJ>

A:Accession: S48207

A:Molecule type: protein

A:Residues: 309-316 <LI2>

A:Accession: S48206

A:Molecule type: protein

A:Residues: 33-37, 'X', 39-40 <LIW>

C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-29/Domain: propeptide #status predicted <PRO>

F:30-559/Domain: t-plasminogen activator #status predicted <MAT>

F:30-308/Domain: t-plasminogen activator chain A #status predicted <ACH>

F:38-75/Domain: fibronectin type I repeat homology <IFR>

F:83-116/Domain: EGF homology <EGF>

F:124-205/Domain: kringle homology <KRI>

F:213-294/Domain: kringle homology <KR2>

F:309-559/Domain: t-plasminogen activator chain B #status predicted <BCH>

F:309-553/Domain: trypsin homology <TRY>

F:38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,29

F:149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted

F:355,404,510/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 100.0%; Pred. No. 5.9e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206
 |||||
 Db 504 DACQDSGGPLVC 516

RESULT 9

UKHUT

t-plasminogen activator (EC 3.4.21.68) precursor [validated] - human
 N;Alternate names: t-PA; tissue plasminogen activator

C;Species: Homo sapiens (man)

C;Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000

C;Accession: A94004; A23529; J00562; A93293; S02125; A91343; A93951; A51322; A54645; I60

R;NY, T.; Elgh, F.; Lund, B.

Proc. Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984

A;Title: The structure of the human tissue-type plasminogen activator gene: correlation

A;Reference number: A94004; MUID:84298137; PMID:6089198

A;Accession: A94004

A;Molecule type: DNA

A;Residues: 1-562 <NVT>

A;Cross-references: GB:L00141

A;Note: The codon given for residue 93 (ACC) is inconsistent with the authors' translation

R;Friedman, Degen, S.J.; Rajput, B.; Reich, E.

J. Biol. Chem. 261, 6972-6985, 1986

A;Title: The human tissue plasminogen activator gene.

A;Reference number: A23529; MUID:86196143; PMID:3009482

A;Accession: A23529

A;Molecule type: DNA

A;Residues: 1-562 <DEG>

A;Cross-references: GB:K03021; NID:G339817; PIDN:AAA98809.1; PID:G339818

R;Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuda, S.; Higashio, K.

Agric. Biol. Chem. 55, 1225-1232, 1991

A;Title: Purification and characterization of tissue plasminogen activator secreted by H

A;Reference number: J00562; MUID:91291340; PMID:1368681

A;Accession: J00562

A;Molecule type: mRNA

A;Residues: 31-562 <ITA>

A;Cross-references: DBJ:D01096; NID:G220128; PIDN:BAA00881.1; PID:G441174

A;Experimental source: embryonic lung fibroblast IMR-90 cells

A;Note: part of this sequence, including the amino end of the mature protein, was confir

R;Pennica, D.; Holmes, W.E.; Kohr, W.O.; Harkins, R.N.; Vehar, G.A.; Ward, C.A.; Bennet

Nature 301, 214-221, 1983

A;Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Esche

A;Reference number: A93293; MUID:83115262; PMID:6337343

A;Accession: A93293

A;Molecule type: mRNA

A;Residues: 1-562 <PEN>

A;Cross-references: GB:L00141

A;Experimental source: melanoma cells

R;Sasaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.

Nucleic Acids Res. 16, 5695, 1988

A;Title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fe

A;Reference number: S02125; MUID:88262579; PMID:3133640

A;Accession: S02125

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-562 <SAS>

A;Cross-references: EMBL:X07193; NID:G37243; PIDN:CAA30302.1; PID:G37244

A;Experimental source: fetal lung cells

R;Kiglati, H.; Isegawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Ma

FEBS Lett. 189, 145-149, 1985

A;Title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen

A;Reference number: A91343; MUID:85285620; PMID:3896853

A;Accession: A91343

A;Molecule type: mRNA

A;Residues: 1-38, G', 86-433, E', 435-562 <XAG>

A;Experimental source: Detroit 562 cells; ATCC 138

R;Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.

Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983

A;Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activ

A;Reference number: A93951; MUID:83169656; PMID:6572897

A;Accession: A93951

A;Molecule type: mRNA

A;Residues: 251-358 <EDL>

A;Experimental source: melanoma cells
 R;Pohl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.

Biochemistry 23, 3701-3707, 1984

A;Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived differences.

A;Reference number: A90488; MUID:85000468; PMID:6433976

A;Contents: annotation; melanoma cells, partial sequence of residues 36-562, active an

R;Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.

FEBS Lett. 168, 29-32, 1984

A;Title: Differences between uterine and melanoma forms of tissue plasminogen activat

A;Reference number: A91322; MUID:84158956; PMID:6538514

A;Accession: A91322

A;Molecule type: protein

A;Residues: 33-45;311-320 <POH>

A;Experimental source: uterus

A;Note: in the uterus, cleavage of the activation peptide may also occur after 38-Gln

R;van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.

J. Biol. Chem. 261, 14214-14218, 1986

A;Reference number: A37567; MUID:87033611; PMID:3021732

A;Contents: annotation; fibrin binding site

R;Verneijlen, J.H.; Caspers, M.F.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; En

EMBO J. 5, 3525-3530, 1986

A;Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen

A;Reference number: A37568; MUID:87161761; PMID:3030730

A;Contents: annotation; fibrin binding site

R;Dodd, I.; Nunn, B.; Robinson, J.H.

Thromb. Haemost. 59, 523-528, 1988

A;Title: Isolation, identification and pharmacokinetic properties of human tissue-type

A;Reference number: A60902; MUID:89044681; PMID:3142086

A;Contents: annotation; novel forms of expressed recombinant t-PA

R;Harris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Emtage, J.S.; Opdenakker, G

Mol. Biol. Med. 3, 279-292, 1986

A;Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its e

A;Reference number: A54645; MUID:86284200; PMID:3090401

A;Accession: A54645

A;Molecule type: mRNA

A;Residues: 1-562 <HAR>

A;Cross-references: GB:W15518; NID:G190031; PIDN:AAA60111.1; PID:G190032

A;Note: parts of this sequence were confirmed by peptide sequencing

R;Reddy, V.B.; Garramone, A.J.; Sabak, H.; Wei, C.

DNA 6, 461-472, 1987

A;Title: Expression of human uterine tissue-type plasminogen activator in mouse cells

A;Reference number: I60110; MUID:88054470; PMID:2824147

A;Accession: I60110

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-562 <RES>

A;Cross-references: GB:M18182; NID:G340176; PIDN:AAA36800.1; PID:G340177

R;Fisher, R.; Waller, E.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.

J. Biol. Chem. 260, 11223-11230, 1985

A;Title: Isolation and characterization of the human tissue-type plasminogen activat

A;Reference number: I55232; MUID:85289338; PMID:3161893

A;Accession: I55232

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-36 <RES>

A;Cross-references: GB:W11890; NID:G339837; PIDN:AAA61213.1; PID:G339839

C;Comment: Cleavage by plasmin or trypsin produces two chains held together by a sing

C;Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond.

C;Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repea

C;Genetics:

A;Gene: GDB:PLAT

A;Cross-references: GDB:119496; OMIM:173370

A;Map position: 8p12-8p12

A;Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3;

C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat

C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-32/Domain: propeptide #status predicted <PRO>

F;33-562/Product: t-plasminogen activator #status experimental <MAT>

F;33-310/Product: t-plasminogen activator chain A #status experimental <ACH>

F;41-78/Domain: fibronectin type I repeat

F;86-119/Domain: EGF homology <EGF>

F:127-208/Domain: kringles homology <KR1>
 F:215-296/Domain: kringles homology <KR2>
 F:311-562/Product: t-plasminogen activator chain B #status experimental <BCH>
 F:311-556/Domain: trypsin homology <TRY>
 F:41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203,215-296,236-278,267-291,299-4
 F:152,483/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:219/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F:310-311/Cleavage site: Arg-Ile (plasmin, trypsin) #status experimental
 F:357,406/Active site: His, Asp #status predicted
 F:513/Active site: Ser #status experimental

Query Match 5.2%; Score 13; DB 1; Length 562;
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQSDSGGPLVC 206
 |||||
 Db 507 DACQSDSGGPLVC 519

RESULT 10
 S45281
 coagulation factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)
 N/Alternate names: Hageman factor (activated)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 10-Apr-1995 #sequence_revision 22-Apr-1995 #text_change 21-Jan-2000
 C/Accession: S45281; A61329
 R/Shibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
 Biochim. Biophys. Acta 1206, 63-70, 1994
 A/Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): comp
 A/Reference number: S45281; MUID:94242782; PMID:8186251
 A/Accession: S45281
 A/Molecule type: mRNA
 A/Residues: 1-593 <SHL>
 A/Cross-references: GB:S70164
 A/Note: the authors translated the codon GAG for residue 23 as Val, GAG for residue 70 as
 s Pro, CTC for residue 203 as Phe, GTG for residue 247 as Leu, CCG for residue 286 as Gl
 is, and APC for residue 505 as Leu
 R/Fujikawa, K.; Walsh, K.A.; Davie, E.W.
 Biochemistry 16, 2270-2278, 1977
 A/Title: Isolation and characterization of bovine factor XII (Hageman factor).
 A/Reference number: A61329; MUID:77182112; PMID:861210
 A/Accession: A61329
 A/Molecule type: protein
 A/Residues: 10-16, 'X' 18-19;525-550 <FUJ>
 C/Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
 C/Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; monomer; plasma;
 F:37-78/Domain: fibronectin type II repeat homology <1F2>
 F:88-120/Domain: EGF homology <EGF>
 F:125-160/Domain: fibronectin type I repeat homology <FBI>
 F:207-287/Domain: kringles homology <KR>
 F:350-587/Domain: trypsin homology <TRY>
 F:541/Active site: Ser #status predicted

Query Match 5.2%; Score 13; DB 2; Length 593;
 Best Local Similarity 100.0%; Pred. No. 6.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQSDSGGPLVC 206
 |||||
 Db 535 DACQSDSGGPLVC 547

RESULT 11
 S28941
 coagulation factor XIIa (EC 3.4.21.38) - guinea pig (fragment)
 N/Alternate names: Hageman factor
 C/Species: Cavia porcellus (guinea pig)
 C/Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
 C/Accession: S28941
 R/Semba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, H.
 Biochim. Biophys. Acta 1159, 113-121, 1992
 A/Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage si

A/Reference number: S28941; MUID:93003367; PMID:1390917
 A/Accession: S28941
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-603 <SEM>
 A/Cross-references: EMBL:X68615; NID:g49578; PIDN:CAA48600.1; PID:g49579
 C/Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homolo
 C/Keywords: hydrolase; serine proteinase
 F:46-87/Domain: fibronectin type II repeat homology <1F2>
 F:134-169/Domain: fibronectin type I repeat homology <FBI>
 F:177-208/Domain: EGF homology <EGF>
 F:216-294/Domain: kringles homology <KR>
 F:359-597/Domain: trypsin homology <TRY>

Query Match 5.2%; Score 13; DB 2; Length 603;
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQSDSGGPLVC 206
 |||||
 Db 545 DACQSDSGGPLVC 557

RESULT 12
 KFHU12
 coagulation factor XIIa (EC 3.4.21.38) precursor [validated] - human
 N/Alternate names: Hageman factor (activated)
 C/Species: Homo sapiens (man)
 C/Date: 27-Nov-1985 #sequence_revision 30-Jun-1991 #text_change 08-Dec-2000
 C/Accession: A29411; A36814; A00930; A25191; A22248; A21037
 R/Cool, D.E.; MacGillivray, R.T.A.
 J. Biol. Chem. 262, 13662-13673, 1987
 A/Title: Characterization of the human blood coagulation factor XII gene. Intron/exon
 A/Reference number: A29411; MUID:88007593; PMID:2888762
 A/Accession: A29411
 A/Molecule type: DNA
 A/Residues: 1-615 <CO>
 A/Cross-references: GB:M17466; GB:J02807; NID:g180355; PIDN:AA859490.1; PID:g180357
 R/Tripodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R.
 Nucleic Acids Res. 14, 3146, 1986
 A/Title: cDNA sequence coding for human coagulation factor XII (Hageman).
 A/Reference number: A26814; MUID:86176794; PMID:3754331
 A/Accession: A26814
 A/Molecule type: mRNA
 A/Residues: 4-615 <TRI>
 A/Cross-references: GB:M31315; NID:g182291; PIDN:AAA70225.1; PID:g182292
 R/Cool, D.E.; Edgell, C.J.S.; Louie, G.V.; Zoller, M.J.; Brayer, G.D.; MacGillivray, R.
 J. Biol. Chem. 260, 13666-13676, 1985
 A/Title: Characterization of human blood coagulation factor XII cDNA. Prediction of t
 A/Reference number: A00930; MUID:86033830; PMID:3877053
 A/Accession: A00930
 A/Molecule type: mRNA
 A/Residues: 14-332, 'S' 334-615 <CO2>
 A/Cross-references: GB:M11723; NID:g180358; PIDN:AAA51986.1; PID:g180359
 R/Que, B.G.; Davie, E.W.
 Biochemistry 25, 1525-1528, 1986
 A/Title: Characterization of a cDNA coding for human factor XII (Hageman factor).
 A/Reference number: A25191; MUID:86216049; PMID:3011063
 A/Accession: A25191
 A/Molecule type: mRNA
 A/Residues: 146-378, 'G' 380-615 <QUE>
 A/Cross-references: GB:M13147; NID:g180360; PIDN:AAA70224.1; PID:g180361
 R/McMullen, B.A.; Fujikawa, K.
 J. Biol. Chem. 260, 5328-5341, 1985
 A/Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated
 A/Reference number: A22248; MUID:85182674; PMID:3886654
 A/Accession: A22248
 A/Molecule type: protein
 A/Residues: 20-379 <MCM>
 R/Fujikawa, K.; McMullen, B.A.
 J. Biol. Chem. 258, 10924-10933, 1983
 A/Title: Amino acid sequence of human beta-factor XIIa.
 A/Reference number: A21037; MUID:83291041; PMID:6604055

```
A;Accession: A21037
A;Molecule type: protein
A;Residues: 354-362;373-615 <FU>
R;Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A;Title: O-linked fucose is present in the first epidermal growth factor domain of factor XIII
A;Reference number: A44606; MUID:92184750; PMID:1544894
A;Contents: annotation; carbohydrate binding site
C;Genetics:
A;Gene: GDB:F12
A;Cross-references: GDB:119892; OMIM:234000
A;Map position: 5q34-qter
A;Introns: 19/3; 72/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 511/1
C;Complex: factor XII, prekallikrein, and HMW kininogen form a complex bound to anionic site
C;Function:
A;Description: factor XIIa catalyzes the proteolytic activation of plasminogen, plasminogen activator, and fibrinolysis
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology; signal sequence; status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-372,373-615/Product: coagulation factor XIIa, alpha form #status experimental <A12>
F;47-88/Domain: fibronectin type II repeat homology <PB2>
F;98-130/Domain: EGF homology <EG1>
F;135-170/Domain: fibronectin type I repeat homology <IF1>
F;178-209/Domain: EGF homology <EG2>
F;217-295/Domain: kringle homology <KRG>
F;298-356/Region: proline-rich
F;354-362,373-615/Product: coagulation factor XIIa, beta form #status experimental <B12>
F;373-609/Domain: trypsin homology <TRY>
F;98-110,104-119,121-130,135-163,161-170,178-189,183-198,200-209,217-295,238-277,266-290
F;109/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;249,433/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;299,305,328,329,337/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;308/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;412,461,563/Active site: His, Asp, Ser #status predicted

Query Match          5.2%; Score 13; DB 1; Length 615;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDGGGGLVLC 206
Db 557 DACQDGGGGLVLC 569

RESULT 13
T30337
polyprotein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003
C;Accession: T30337
R;Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A;Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from Xenopus laevis
A;Reference number: Z20829
A;Accession: T30337
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1524 <YAN>
A;Cross-references: EMBL:U81290; NID:G2981640; PID:G2981641; PIDN:AAC24717.1
C;Superfamily: tryosin related polyprotein; trypsin homology

Query Match          5.2%; Score 13; DB 2; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDGGGGLVLC 206
Db 762 DACQDGGGGLVLC 774

RESULT 14
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S54115
complement factor D (EC 3.4.21.46) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 19-May-2000
C;Accession: S54115
R;Nicolas, N.
submitted to the EMBL Data Library, April 1995
A;Reference number: S54115
A;Accession: S54115
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-191 <NIC>
A;Cross-references: EMBL:Z49059; NID:G773264; PIDN:CAA88444.1; PID:G773265
C;Superfamily: trypsin; trypsin homology
C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F;1-181/Domain: trypsin homology (fragment) <TRY>

Query Match          4.8%; Score 12; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 GDSGGPLVCGGV 209
Db 139 GDSGGPLVCGGV 150

RESULT 15
S65465
trypsin-like proteinase (EC 3.4.21.-) precursor - flesh fly (Sarcophaga bullata)
C;Species: Sarcophaga bullata
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S65465; S65403
R;Borovsky, D.; Janssen, I.; Vanden Broeck, J.; Huybrechts, R.; Verhaert, P.; de Bondt, J.
Eur. J. Biochem. 237, 279-287, 1996
A;Title: Molecular sequencing and modeling of Neobellieria bullata trypsin. Evidence
A;Reference number: S65403; MUID:96203936; PMID:8620885
A;Accession: S65465
A;Molecule type: mRNA
A;Residues: 1-254 <BOR>
A;Cross-references: EMBL:X94691; NID:gl177315; PIDN:CAA64354.1; PID:gl177316
A;Accession: S65403
A;Molecule type: protein
A;Residues: 27-36 <BOW>
A;Note: 27-Leu, 35-Leu were also found
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; signal sequence #status predicted <SIG>
F;1-16/Domain: signal sequence #status predicted <PRO>
F;17-254/Product: trypsin #status experimental <MAT>
F;27-247/Domain: trypsin homology <TRY>
F;53-69,154-158,195-238,204-228/Disulfide bonds: #status predicted
F;68,113,208/Active site: His, Asp, Ser #status predicted

Query Match          4.8%; Score 12; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDGGGGLV 205
Db 202 DACQDGGGGLV 213

Search completed: June 15, 2004, 16:25:50
Job time : 21 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 16:17:12 ; Search time 60 Seconds
(without alignments)
1167.863 Million cell updates/sec

Title: US-10-006-856A-194
Perfect score: 248
Sequence: 1 MGLSIFLLCVLGLSQAATP.....GYTYICKYVDWIRIMRN 248

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 segs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	100.0	248	3	AAB21304 Human KLK
2	248	100.0	248	3	AAB24428 Human PRO
3	248	100.0	248	3	AAB24032 Human PRO
4	248	100.0	248	3	AAY99393 Human PRO
5	248	100.0	248	4	AAM23994 Human EST
6	248	100.0	248	4	AAB66142 Protein o
7	248	100.0	248	6	AAB33635 Novel hum
8	248	100.0	248	7	ABO44488 Human sec
9	248	100.0	248	7	ABO33512 Novel hum
10	248	100.0	248	7	ADCI18063 Human PRO
11	248	100.0	248	7	ADD70709 Human sec
12	248	100.0	248	7	ADD39786 Human sec
13	248	100.0	248	7	ADD70232 Human sec
14	248	100.0	248	7	ADD38353 Human sec
15	248	100.0	248	7	ADD39309 Human sec
16	248	100.0	248	7	ADD38832 Human sec
17	248	100.0	248	7	ADD40263 Human sec
18	248	100.0	248	7	ADE50484 Human sec
19	248	100.0	248	7	ADE20096 Human sec
20	248	100.0	248	7	ADE50007 Human sec
21	248	100.0	248	7	ADE21565 Human sec
22	235	94.8	254	3	AAB21303 Human KLK
23	235	94.8	254	5	ABG66676 Human nov
24	184	74.2	184	3	AAB21301 Human KLK
25	182	73.4	248	6	AAB29516 Human kal

ALIGNMENTS

RESULT 1

AAB21304
ID AAB21304 standard; protein; 248 AA.
XX
AC AAB21304;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human KLK-L5 protein #4.
XX
KW Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6;
KW kallikrein-like protein; serine protease; cytosolic; cancer;
KW prostrate cancer.
XX
OS Homo sapiens.
XX
PN WO200053776-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-CA000258.
XX
PR 11-MAR-1999; 99US-0124260P.
PR 01-APR-1999; 99US-0127386P.
21-JUL-1999; 99US-0144919P.
PA (MOUN) MOUNT SINAI HOSPITAL.
XX
PI Yousef GM, Diamandis EP;
DR WPI; 2000-587440/55.
N-PSDB; AAB95944.
XX
PT New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L protein mediated disorders, especially cancer.
PS Claim 12; Page 172; 184pp; English.
CC The present sequence is one of four alternatively spliced kallikrein-like proteins encoded by the human KLK-L4 gene. Kallikreins and kallikrein-like proteins are a subgroup of the serine protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of cancers, especially prostate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used

26 93 37.5 162 2 AAY28642 Human sec
27 65 26.2 111 3 AAB21302 Human KLK
28 14 5.6 562 1 AAP70474 Sequence
29 13 5.2 30 3 AAB08953 Human sec
30 13 5.2 70 5 AAU76373 Human Mar
31 13 5.2 107 5 ABP09500 Human ORF
32 13 5.2 113 7 ADC31388 Human nov
33 13 5.2 117 1 AAP81986 Chain 2 o
34 13 5.2 187 3 AAY72094 Human ser
35 13 5.2 187 5 ABG30791 Human ser
36 13 5.2 187 5 AAE17922 Human gen
37 13 5.2 199 5 AAU77550 Membrane-
38 13 5.2 212 2 AAY28590 Human Fac
39 13 5.2 214 4 AAG79215 Consensus
40 13 5.2 216 6 ABO00751
41 13 5.2 226 5 AAE21442 Human try
42 13 5.2 226 6 ABG75786 Trypsin d
43 13 5.2 227 5 AAE14342 Human pro
44 13 5.2 227 6 ABG75785 Trypsin d
45 13 5.2 228 7 AAE39994 Human adi

CC to treat conditions mediated by the kallikrein-like proteins
 XX
 SQ Sequence 248 AA;

Query Match 100.0%; Score 248; DB 3; Length 248;
 Best Local Similarity 100.0%; Pred. No. 8.4e-182;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 60
 DB 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 60
 QY 61 AHCSGRYWRVLRGHSLSQLDWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLPVRV 120
 DB 61 AHCSGRYWRVLRGHSLSQLDWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLPVRV 120
 QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPPFDLLQCLNLSIVSHATCHGVYVPGRI 180
 DB 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPPFDLLQCLNLSIVSHATCHGVYVPGRI 180
 QY 181 TSNMVCAGVPGQDACQDGGPLVCGVLOGLVSWGSGVPCQDGIPIGVYTYICKYVDW 240
 DB 181 TSNMVCAGVPGQDACQDGGPLVCGVLOGLVSWGSGVPCQDGIPIGVYTYICKYVDW 240
 QY 241 IRMIMRNN 248
 DB 241 IRMIMRNN 248

RESULT 2

AAB24428
 ID AAB24428 standard; protein; 248 AA.

AC AAB24428;

XX 07-NOV-2000 (first entry)

DE Human PRO1303 protein sequence SEQ ID NO:203.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
 KW cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1998; 98WO-US025108.

XX 16-DEC-1998; 98US-0112850P.

XX 12-JAN-1999; 99US-0115554P.

XX 08-MAR-1999; 99WO-US0005028.

XX 12-MAR-1999; 99US-0123957P.

XX 28-APR-1999; 99US-0131445P.

XX 14-MAY-1999; 99US-0134287P.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 26-JUL-1999; 99US-0144758P.

XX 01-SEP-1999; 99US-0145698P.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 05-OCT-1999; 99WO-US021547.

XX 29-OCT-1999; 99WO-US023089.

XX 99US-0162506P.

XX (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
 PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
 XX Smith V, Watanabe CK, Williams PM, Wood WI;

XX WPI; 2000-412154/35.

DR N-PSDB; AAA77671.

XX Claim 72; Fig 82; 315pp; English.

PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
 and treating atherosclerosis, endotheelial or angiogenic
 disorders in mammals.

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Sequence 248 AA;

Query Match 100.0%; Score 248; DB 3; Length 248;

Best Local Similarity 100.0%; Pred. No. 8.4e-182;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 60

DB 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 60

QY 61 AHCSGRYWRVLRGHSLSQLDWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLPVRV 120

DB 61 AHCSGRYWRVLRGHSLSQLDWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLPVRV 120

QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPPFDLLQCLNLSIVSHATCHGVYVPGRI 180

DB 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPPFDLLQCLNLSIVSHATCHGVYVPGRI 180

QY 181 TSNMVCAGVPGQDACQDGGPLVCGVLOGLVSWGSGVPCQDGIPIGVYTYICKYVDW 240

DB 181 TSNMVCAGVPGQDACQDGGPLVCGVLOGLVSWGSGVPCQDGIPIGVYTYICKYVDW 240

QY 241 IRMIMRNN 248

DB 241 IRMIMRNN 248

RESULT 3

AAB24032

ID AAB24032 standard; protein; 248 AA.

XX AAB24032;

XX 25-JAN-2001 (first entry)

XX Human PRO1303 protein sequence SEQ ID NO:33.

XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;

XX identification; tumourigenesis; anticancer; detection.

XX Homo sapiens.

XX WO200053750-A1.

XX 14-SEP-2000.

PD

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XX PF 02-DEC-1999; 99WO-US028551.
XX PF 08-MAR-1999; 99WO-US005028.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 29-OCT-1999; 99US-0162506P.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1999; 99WO-US028634.
XX PA (GETH ) GENENTECH INC.
XX XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WL;
XX WPI; 2000-594320/56.
XX DR N-PSDB; AAC58114.
XX XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
XX PT the growth of tumors in mammals, and to identify inhibitors of PRO
XX PT polypeptide activity or expression.
XX PS Claim 61; Fig 24; 226pp; English.
XX CC The present invention describes an antibody that binds to a human protein
XX CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
XX CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
XX CC PRO4407; PRO1555; PRO1036; PRO2038; and PRO2262. (I) has anticancer
XX CC activity and can be used to diagnose tumours in mammals, by detecting
XX CC complex formation when the antibody is contacted with test cells.
XX CC Increased expression of genes encoding (I) can also be detected to
XX CC diagnose tumours. Agents which inhibit the activity of (I), especially
XX CC the antibodies, or an antisense oligonucleotide which hybridises to genes
XX CC encoding (I), can be used to inhibit tumour growth, preferably by
XX CC inducing cell death. Methods from the present invention can be used to
XX CC identify compounds which inhibit the biological activity of (I). AAC58019
XX CC to AAC58102 represent PCR primers and hybridisation probes used in
XX CC examples from the present invention for human PRO sequences. AAC58103 to
XX CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
XX CC protein sequences given in the exemplification of the present invention
XX SQ Sequence 248 AA;

Query Match 100.0%; Score 248; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVILGSLQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 60
Db 1 MGLSIFLLLCVILGSLQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 60
QY 61 AHCSGRYVWRLGEHSLDQTEQIRHSGFSVTHPGYLGASTSHHDLRLRLRPVRV 120
Db 61 AHCSGRYVWRLGEHSLDQTEQIRHSGFSVTHPGYLGASTSHHDLRLRLRPVRV 120
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPFDDLLQCLNLSVSHATCGVYVPGRI 180
Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPFDDLLQCLNLSVSHATCGVYVPGRI 180
QY 181 TSNMVCAGVPGQDAGCGSGGLVCGVLCGLVSGVSGPCQDGPVYVYI CKYVDW 240
Db 181 TSNMVCAGVPGQDAGCGSGGLVCGVLCGLVSGVSGPCQDGPVYVYI CKYVDW 240
QY 241 IRMIMRNN 248
Db 241 IRMIMRNN 248

RESULT 4
ID AAY99393
XX AC AAY99393 standard; protein; 248 AA.
XX AC AAY99393;
XX DT 08-AUG-2000 (first entry)

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XX DE Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.
XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
XX KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX XX Homo sapiens.
XX OS WO2000012708-A2.
XX FN 09-MAR-2000.
XX PD 01-SEP-1999; 99WO-US020111.
XX XX 01-SEP-1998; 99US-0098716P.
XX PR 01-SEP-1998; 99US-0098749P.
XX PR 02-SEP-1998; 99US-0098750P.
XX PR 02-SEP-1998; 99US-0098803P.
XX PR 02-SEP-1998; 99US-0098821P.
XX PR 02-SEP-1998; 99US-0098843P.
XX PR 02-SEP-1998; 99US-0099536P.
XX PR 02-SEP-1998; 99US-009956P.
XX PR 02-SEP-1998; 99US-009958P.
XX PR 02-SEP-1998; 99US-0099602P.
XX PR 02-SEP-1998; 99US-0099642P.
XX PR 10-SEP-1998; 99US-0099741P.
XX PR 10-SEP-1998; 99US-0099754P.
XX PR 10-SEP-1998; 99US-0099763P.
XX PR 10-SEP-1998; 99US-0099792P.
XX PR 10-SEP-1998; 99US-0099808P.
XX PR 10-SEP-1998; 99US-0099812P.
XX PR 10-SEP-1998; 99US-0099815P.
XX PR 10-SEP-1998; 99US-0099816P.
XX PR 15-SEP-1998; 99US-0100385P.
XX PR 15-SEP-1998; 99US-0100388P.
XX PR 15-SEP-1998; 99US-0100390P.
XX PR 16-SEP-1998; 99US-0100584P.
XX PR 16-SEP-1998; 99US-0100627P.
XX PR 16-SEP-1998; 99US-0100661P.
XX PR 16-SEP-1998; 99US-0100662P.
XX PR 16-SEP-1998; 99US-0100664P.
XX PR 17-SEP-1998; 99US-0100683P.
XX PR 17-SEP-1998; 99US-0100684P.
XX PR 17-SEP-1998; 99US-0100710P.
XX PR 17-SEP-1998; 99US-0100711P.
XX PR 17-SEP-1998; 99US-0100913P.
XX PR 17-SEP-1998; 99US-0100930P.
XX PR 18-SEP-1998; 99US-0100848P.
XX PR 18-SEP-1998; 99US-0100849P.
XX PR 18-SEP-1998; 99US-0101014P.
XX PR 18-SEP-1998; 99US-0101068P.
XX PR 18-SEP-1998; 99US-0101071P.
XX PR 22-SEP-1998; 99US-0101279P.
XX PR 23-SEP-1998; 99US-0101471P.
XX PR 23-SEP-1998; 99US-0101472P.
XX PR 23-SEP-1998; 99US-0101474P.
XX PR 23-SEP-1998; 99US-0101475P.
XX PR 23-SEP-1998; 99US-0101476P.
XX PR 23-SEP-1998; 99US-0101477P.
XX PR 24-SEP-1998; 99US-0101479P.
XX PR 24-SEP-1998; 99US-0101738P.
XX PR 24-SEP-1998; 99US-0101741P.
XX PR 24-SEP-1998; 99US-0101743P.
XX PR 24-SEP-1998; 99US-0101915P.
XX PR 24-SEP-1998; 99US-0101916P.
XX PR 29-SEP-1998; 99US-0102207P.
XX PR 29-SEP-1998; 99US-0102240P.
XX PR 29-SEP-1998; 99US-0102307P.
XX PR 29-SEP-1998; 99US-0102330P.
XX PR 29-SEP-1998; 99US-0102331P.
XX PR 30-SEP-1998; 99US-0102484P.
XX PR 30-SEP-1998; 99US-0102487P.
XX PR 30-SEP-1998; 99US-0102570P.

```


XX WPI; 2001-476164/51.
DR N-PSDB; AAH98653.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
XX Claim 20; Page 1048-1049; 1275pp; English.
PS
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
XX protein of the invention
XX
SQ Sequence 248 AA;
Query Match 100.0%; Score 248; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGLSIFLLLCVLGSLQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
QY 61 AHCSGSRYWVRIGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPVRV 120
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QY 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPNPFDDLLQCLNLSIVSHATCHGVYPGR 180
Db 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPNPFDDLLQCLNLSIVSHATCHGVYPGR 180
QY 181 TSNMVCAGVPQDACCQDSGGLVCGVQLGLVSGSVGPGQDIPGVYIICKYVDW 240
Db 181 TSNMVCAGVPQDACCQDSGGLVCGVQLGLVSGSVGPGQDIPGVYIICKYVDW 240
QY 241 IRMIMRNN 248
Db 241 IRMIMRNN 248
RESULT 6
AAB66142
ID AAB66142 standard; protein; 248 AA.
XX
XX AAB66142;
AC
XX
DT 02-APR-2001 (first entry)
XX
DE Protein of the invention #54.
XX
XX Secreted; transmembrane; gene therapy.
XX
XX Unidentified.
XX
XX WO200078961-A1.
PN
XX
PD 28-DEC-2000.
XX
XX 18-FEB-2000; 2000WO-US004342.
PF
XX 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Botstein D, Deanoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoletti NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2001-071395/08.
DR
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
PT
XX
XX Claim 1; Fig 108; 787pp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
SQ Sequence 248 AA;
Query Match 100.0%; Score 248; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSIFLLLCVLGSLQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
Db 1 MGLSIFLLLCVLGSLQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
QY 61 AHCSGSRYWVRIGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPVRV 120
Db 61 AHCSGSRYWVRIGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPVRV 120
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPNPFDDLLQCLNLSIVSHATCHGVYPGR 180
Db 121 TSSVQPLPLPNDCATAGTECHVSGWGI TNHPNPFDDLLQCLNLSIVSHATCHGVYPGR 180
QY 181 TSNMVCAGVPQDACCQDSGGLVCGVQLGLVSGSVGPGQDIPGVYIICKYVDW 240
Db 181 TSNMVCAGVPQDACCQDSGGLVCGVQLGLVSGSVGPGQDIPGVYIICKYVDW 240
QY 241 IRMIMRNN 248
Db 241 IRMIMRNN 248
RESULT 7
ABO33635
ID ABO33635 standard; protein; 248 AA.
XX
XX ABO33635;
AC
XX
XX 17-SEP-2003 (first entry)
DT
XX
XX Novel human secreted and transmembrane protein PRO1303.
DE
XX
XX Human; secreted and transmembrane protein; PRO; angiogenesis;
KW endothelial cell proliferation; wound healing; immune response;
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
KW cardiac insufficiency disorder; calcium flux; inflammation;
KW vascular endothelial growth factor-stimulated proliferation;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
KW pancreatic beta-cell precursor cell differentiation; thalassemias;
KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
KW

KW cartilage disorder; sports injury; arthritis.
XX Homo sapiens.
OS US2003073130-A1.
PN 17-APR-2003.
PD
XX
XX
PF 11-DEC-2001; 2001US-00015869.
XX
XX 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 02-SEP-1998; 98US-0099536P.
PR 03-SEP-1998; 98US-0099596P.
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PR 01-OCT-1998; 98US-0102684P.
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PR 07-OCT-1998; 98US-0103314P.
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PR 21-OCT-1998; 98US-0105104P.
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PR 18-NOV-1998; 98US-0108848P.
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PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114233P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99WO-US029674P.
PR 23-JUN-1999; 99US-0141017P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US008520.
 PR 01-MAR-2001; 2001WO-US008666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NP, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams FM, Wood WI;
 XX WPI; 2003-585293/55.
 DR N-PSDB; ACD68378.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
 PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
 PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

Query Match 100.0%; Score 248; DB 6; Length 248;
 Best Local Similarity 100.0%; Pred. No. 8.4e-182;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQFQVGLFEGTSLRCGGVLIDHRWLTA 60
 Db 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQFQVGLFEGTSLRCGGVLIDHRWLTA 60
 QY 61 AHCSGRYVRLGHSLSQDWTQEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
 Db 61 AHCSGRYVRLGHSLSQDWTQEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
 QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
 Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
 QY 181 TSNMVCAGVPGQDACGDSGGLVCGGVVQLGLVSGSVGPGQDGPVYTYICKYVDW 240
 Db 181 TSNMVCAGVPGQDACGDSGGLVCGGVVQLGLVSGSVGPGQDGPVYTYICKYVDW 240
 QY 241 IRMIMRNN 248
 Db 241 IRMIMRNN 248

RESULT 8
 ABO44488
 ID ABO44488 standard; protein; 248 AA.
 XX ABO44488;
 AC
 XX 01-OCT-2003 (first entry)
 DT
 XX Human secreted/transmembrane protein PRO1303.
 DE
 XX Human; secreted protein; transmembrane protein; PRO; vulnerary; cardiant;
 KW

KW antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
 KW adrenal cortical capillary; endothelial cell growth; wound healing;
 KW stimulated T-lymphocyte proliferation; immune response suppression;
 KW neonatal heart hypertrophy; cardiac insufficiency disorder;
 KW vascular endothelial growth factor; inflammation; mononuclear cell;
 KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
 KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
 KW sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX US2003044841-AL.
 PN 06-MAR-2003.
 XX
 PD 06-DEC-2001; 2001US-00006856.
 PF
 XX 01-SEP-1998; 98US-0098716P.
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 PR 02-SEP-1998; 98US-0098803P.
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PR 10-NOV-1998; 98US-0107783P.
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PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144756P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US005884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX
PA (GETH ) GENENTECH INC.
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WFI; 2003-492259/46.
DR N-PSDB; ACH04480.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating various cardiac insufficiency
PT disorders, bone and/or cartilage disorders such as sports injuries and
PT arthritis.
Query Match 100.0%; Score 248; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQFQVGLFEGTSLRCGGVLIDHRWLTA 60
Db 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQFQVGLFEGTSLRCGGVLIDHRWLTA 60
Qy 61 AHCSGRYVRLGEHSLSQLDWTQIRHSGFSVTHPGYLGAOSTSHEHDLRLRLPVRV 120
Db 61 AHCSGRYVRLGEHSLSQLDWTQIRHSGFSVTHPGYLGAOSTSHEHDLRLRLPVRV 120
Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGTNHPNPFDDLOCLNLSIVSHATCHGVYPGRI 180
Db 121 TSSVQPLPLPNDCATAGTECHVSGWGTNHPNPFDDLOCLNLSIVSHATCHGVYPGRI 180
Qy 181 TSNMVCAGVPGQDACQDSGGVLVCGVQLGVLSVSGSVGPGCCQDGIPIGVYTYCKYVDW 240
Db 181 TSNMVCAGVPGQDACQDSGGVLVCGVQLGVLSVSGSVGPGCCQDGIPIGVYTYCKYVDW 240
Qy 241 IRMIMN 248
Db 241 IRMIMN 248
RESULT 9
ABO33512
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ID ABO33512 standard; protein; 248 AA.
XX AC ABO33512;
XX DT 17-SEP-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1303.
XX KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
XX KW tissue typing; chromosome identification; vaccine.
XX OS Homo sapiens.
XX PN US2003073129-A1.
XX PD 17-APR-2003.
XX PF 04-SEP-2001; 2001US-00946374.
XX PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
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PR 03-SEP-1998; 98US-0099569P.
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PR 18-NOV-1998; 98US-0108849P.
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PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.

PR 12-APR-1999; 99US-00284291.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0144758P.
PR 01-SEP-1999; 99US-0145698P.
PR 15-SEP-1999; 99US-02020111.
PR 18-OCT-1999; 99US-02021194.
PR 30-NOV-1999; 99US-00403297.
PR 02-DEC-1999; 99US-0202313.
PR 16-DEC-1999; 99US-02028551.
PR 05-JAN-2000; 99US-02030095.
PR 06-JAN-2000; 2000MO-US000219.
PR 11-FEB-2000; 2000MO-US000376.
PR 18-FEB-2000; 2000MO-US003356.
PR 24-FEB-2000; 2000MO-US004342.
PR 02-MAR-2000; 2000MO-US005004.
PR 15-MAR-2000; 2000MO-US005841.
PR 17-MAY-2000; 2000MO-US006884.
PR 22-MAY-2000; 2000MO-US013705.
PR 30-MAY-2000; 2000MO-US014042.
PR 02-JUN-2000; 2000MO-US014941.
PR 23-AUG-2000; 2000MO-US015264.
PR 24-AUG-2000; 2000MO-US023522.
PR 08-NOV-2000; 2000MO-US023328.
PR 10-NOV-2000; 2000MO-US030952.
PR 01-DEC-2000; 2000MO-US030873.
PR 28-FEB-2001; 2000MO-US032678.
PR 01-MAR-2001; 2001MO-US000520.
PR 01-JUN-2001; 2001MO-US006666.
PR 14-JUN-2001; 2001US-00872035.
PR 20-JUN-2001; 2001MO-US017800.
PR 29-JUN-2001; 2001MO-US019692.
PR 09-JUL-2001; 2001MO-US021066.
PR 2003-585292/55.
PR N-PSDB; ACD68024.
PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX Claim 12; Fig 108; 561pp; English.
XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (I), having at least 80% sequence identity to a sequence
Query Match 100.0%; Score 248; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSIIFLLICVLGSLQATKPIFNGTCGRNSQPQVGLFEGTSLRCGGVLIDHRWYLT 60
Db 1 MGSIIFLLICVLGSLQATKPIFNGTCGRNSQPQVGLFEGTSLRCGGVLIDHRWYLT 60
QY 61 AHCSGSRYWRLGSHLSQLDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPVR 120
Db 61 AHCSGSRYWRLGSHLSQLDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPVR 120
QY 121 TSSVQPLPLNDCATAGTECHVSGWGTNHPNPFDPDLQLCLNLSIVSHATCHGVYPGRI 180
Db 121 TSSVQPLPLNDCATAGTECHVSGWGTNHPNPFDPDLQLCLNLSIVSHATCHGVYPGRI 180
QY 181 TSNMVCAGGVPQDACQDSGGLVCGVLOGLVSWGSGVPCGQDGPVGYTYICKYVDW 240

Db 181 TSNMVCAGGVPQDACQDSGGLVCGVLOGLVSWGSGVPCGQDGPVGYTYICKYVDW 240
QY 241 IRMIMRNN 248
Db 241 IRMIMRNN 248
RESULT 10
ADCL8063
ID ADCL8063 standard; protein; 248 AA.
XX AC ADCL8063;
XX DT 18-DEC-2003 (first entry)
XX DE Human PRO polypeptide #54.
KW Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;
XX genetic disorder.
XX OS Homo sapiens.
XX PN US2003064925-A1.
XX PD 03-APR-2003.
XX PF 10-DEC-2001; 2001US-00013907.
XX PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
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PR 10-SEP-1998; 98US-0098974P.
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PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
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PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 22-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.

[illegible]

Query Match 100.0%; Score 248; DB 7; Length 248;
 Best local similarity 100.0%; Pred. No. 8.4e-182;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVLGLSQAATPKIFNGTEGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
 DB 1 MGLSIFLLLCVLGLSQAATPKIFNGTEGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
 QY 61 AHCSGSRYVWRLGEHSLSDLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
 DB 61 AHCSGSRYVWRLGEHSLSDLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
 QY 121 TSSVQPLPLPNDPCATAGTECHVSGMGITNHPNPPDLLQCLINLSIVSHATCHGVYPGRI 180
 DB 121 TSSVQPLPLPNDPCATAGTECHVSGMGITNHPNPPDLLQCLINLSIVSHATCHGVYPGRI 180
 QY 181 TSNMVCAGGVPGODACQDGGPLVCGGVQLQGLVSWGSGVCGQDGIPIGVYTYICKYVDW 240
 DB 181 TSNMVCAGGVPGODACQDGGPLVCGGVQLQGLVSWGSGVCGQDGIPIGVYTYICKYVDW 240
 QY 241 IRIMMENN 248
 DB 241 IRIMMENN 248

RESULT 12
 ADD39786
 ID ADD39786 standard; protein; 248 AA.
 XX AC ADD39786;
 XX DT 15-JAN-2004 (first entry)
 XX DE Human secreted/transmembrane protein PRO1303.
 XX KW Human; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
 XX OS Homo sapiens.
 XX US2003083462-A1.
 XX PD 01-MAY-2003.
 XX PF 10-DEC-2001; 2001US-00013913.
 XX PR 05-JAN-1999; 99WO-US000106.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.

(GETH) GENENTECH INC.
 Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
 Gao W, Goddard A, Godowski BJ, Grimaldi JC, Gurney AL, Hillan KJ;
 Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 Williams PM, Wood WI;
 WPI; 2003-874602/81.
 N-PSDB; ADD70708.

Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
 PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
 cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
 Claim 12; SEQ ID NO 194; 553pp; English.

The invention relates to an isolated PRO polypeptide (secreted or

PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
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PR 17-NOV-1998; 98US-0108806P.
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PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0144758P.
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PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023528.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-786999/74.

DR N-PSDB; ADD39308.
XX Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
PS Claim 12; SEQ ID NO 194; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 248; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVIGLSQATPKIFNGTECGNSQPVQVGLFEGTSLRCGGVLIDHRWVLT 60
DB 1 MGLSIFLLLCVIGLSQATPKIFNGTECGNSQPVQVGLFEGTSLRCGGVLIDHRWVLT 60

QY 61 AHCSSGSRVWVRLGEHSLDQWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
DB 61 AHCSSGSRVWVRLGEHSLDQWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120

QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180

QY 181 TSNMYCAGGVPGODACQGDGGLVCGVYLGVLVSGVSGPCGQDGPVYTYICKYVDW 240
DB 181 TSNMYCAGGVPGODACQGDGGLVCGVYLGVLVSGVSGPCGQDGPVYTYICKYVDW 240

QY 241 IRMIMENN 248
DB 241 IRMIMENN 248

Search completed: June 15, 2004, 16:23:49
Job time : 61 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 16:12:21 ; Search time 46 Seconds
(without alignments)
1701.055 Million cell updates/sec

Title: US-10-006-856A-194

Perfect score: 1374

Sequence: 1 MGLSIFLLLCVLGLSQAATP.....GVYTYICKYVDWIRIMRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	952.5	69.3	234	11 Q9CV76	Q9cv76 mus musculus
2	627.5	45.7	260	4 Q8Iw69	Q8iW69 homo sapien
3	608	44.3	254	11 Q8CGR4	Q8cgr4 mus musculus
4	601	43.7	275	4 Q8IXD7	Q8ixd7 homo sapien
5	597.5	43.5	249	11 Q9QYN4	Q9qyn4 mus musculus
6	597.5	43.5	276	11 Q9QYN3	Q9qyn3 m hippostas
7	595	43.3	255	4 Q96RQ0	Q96rq0 homo sapien
8	588.5	42.8	293	11 Q9D140	Q9d140 mus musculus
9	588	42.8	276	11 Q8CGR6	Q8cgr6 mus musculus
10	586	42.6	250	11 Q8CGR5	Q8cgr5 mus musculus
11	578	42.1	242	11 Q8QV54	Q8qv54 mus musculus
12	563	41.0	248	13 Q7SZT1	Q7azt1 xenopus lae
13	555	40.4	243	13 Q7SZ06	Q7az06 xenopus lae
14	553.5	40.3	246	11 Q8B301	Q8b301 mus musculus
15	553.5	40.3	253	11 Q91Y82	Q91y82 mus musculus
16	550.5	40.1	247	11 Q9D7Y7	Q9d7y7 mus musculus

17	549.5	40.0	247	11 Q9CPN9	Q9cpn9 mus musculus
18	546.5	39.8	251	11 Q54854	O54854 rattus norv
19	544	39.6	253	4 Q8NSN9	Q8nsn9 homo sapien
20	541.5	39.4	247	11 Q9CPN7	Q9cpn7 mus musculus
21	538.5	39.2	249	11 Q91VE3	Q9ive3 mus musculus
22	536	39.0	246	11 Q9R0T7	Q9rot7 mus musculus
23	536	39.0	246	11 Q7TT42	Q7tt42 mus musculus
24	533	38.8	246	11 Q9Z1R9	Q9zir9 mus musculus
25	532	38.7	246	11 Q9QUK9	Q9qk9 mus musculus
26	525	38.2	240	13 Q98TH0	Q98th0 engraulis j
27	522	38.0	244	13 Q8QW3	Q8ggw3 anguilla ja
28	514.5	37.4	242	13 Q7T1R8	Q7t1r8 pangasius h
29	514	37.4	239	11 Q63275	Q63275 rattus norv
30	513.5	37.4	243	13 Q8AV83	Q8av83 brachydanio
31	513.5	37.4	261	6 Q9NIQ1	Q9niq1 saguinus oe
32	513.5	37.4	278	11 Q99M20	Q99m20 mus musculus
33	511.5	37.2	261	6 Q29474	Q29474 canis famil
34	510.5	37.2	238	13 Q9W7Q6	Q9w7q6 paralichthy
35	509.5	37.1	222	13 Q8AV11	Q8av11 oncorhynch
36	509.5	37.1	235	11 Q63274	Q63274 rattus norv
37	508	37.0	242	13 Q9W7Q7	Q9w7q7 paralichthy
38	507	36.9	244	13 Q42159	Q42159 petromyzon
39	506	36.8	245	13 Q42160	Q42160 petromyzon
40	505	36.8	242	13 Q7SX90	Q7sx90 brachydanio
41	505	36.8	249	13 Q92046	Q92046 dissoatichu
42	504.5	36.7	269	4 Q8IU55	Q8iu55 homo sapien
43	503	36.6	241	13 Q98TG9	Q98tg9 engraulis j
44	502	36.5	249	13 Q9W6K0	Q9w6k0 notothenia
45	501.5	36.5	237	13 Q91515	Q91515 fugu rubrip

ALIGNMENTS

RESULT 1

Q9CV76 PRELIMINARY; PRT; 234 AA.
ID AC Q9CV76;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 2310008B01rik protein (fragment).
GN 2310008B01RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada S.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nitaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RT Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AK009217; BAB26143.1; -.

DR HSP; P00763; LDPO.
DR MEROPS; S01.020; -.
DR MGD; MGI:1916761; 2310008B01Rik.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_SIA.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1
SQ SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;

Query Match 69.3%; Score 952.5; DB 11; Length 234;
Best Local Similarity 70.6%; Pred. No. 4.1e-84;
Matches 166; Conservative 27; Mismatches 41; Indels 1; Gaps 1;

QY 14 LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYYVRLG 73
Db 1 LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYYVRLG 59

QY 74 EHSLSQDWTQIRHSGFVSHTPGVGLGASTSHEHDLRLRLRLPVRVTSVQPIPLPND 133
Db 60 EHSLSQDWTQIRHSGFVSHTPGVGLGASTSHEHDLRLRLRLPVRVTSVQPIPLPND 133

QY 134 ATAGTECHVSGWGTINHPNRPFDLLQCLNLSIVSHATCHGVYPRITSNMVCAGVPGQ 193
Db 120 VTTGAMCHVSGWGTINHPNRPFDLLQCLNLSIVSHATCHGVYPRITSNMVCAGVPGQ 179

QY 194 DACQDGGPLVCGGVGLQGLVSGVSGPCGGQIGIPGVVYICKYVTVYICKYVDMIRNN 248
Db 180 DACQDGGPLVCGGVGLQGLVSGVSGPCGGQIGIPGVVYICKYVTVYICKYVDMIRNN 234

RESULT 2
Q81W69 PRELIMINARY; PRT; 260 AA.
ID Q81W69 AC
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strauberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040887; AAH40887.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_SIA.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hypothetical protein.
SQ SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;

Query Match 45.7%; Score 627.5; DB 4; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.4e-52;
Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;

QY 5 IFLL--CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61
Db 13 MFLLLLGGAWAGHSRAQEDVGLGHECPHSPQWQAALFQCGQLCGVLLVGGNWLTA 72

QY 62 HCSGRYVRLGHEHSLSQLDWTQIRHSGFVSHTPGVGLGAST-SHEHDLRLRLRLPVRV 120
Db 73 HCKKPKYTVRLGDHSLQNKDQPEQEIFVQSIHPHCNSSDVEDHEDMLQLRDQASL 132

QY 121 TSSVQPIPLPNDCATAGTECHVSGWGTINHPNRPFDLLQCLNLSIVSHATCHGVYPR 180
Db 133 GSKVKPISLADHCTQPGQCKCTVSGWGTVTSPTRENFPTLNCARVKIPFQKKCEDAYPGQ 192

QY 181 TSNMVCAGVPGQDACQDGGPLVCGGVGLQGLVSGVSGPCGGQIGIPGVVYICKYVDM 240
Db 193 TDVNVVAGSSKGAATCGDGGPLVCGALQGITSWGSS-DPCGRSDKPGVTTNICRYLDW 251

QY 241 IRMIM 245
Db 252 IKKII 256

RESULT 3
Q8CGR4 PRELIMINARY; PRT; 254 AA.
ID Q8CGR4 AC
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prostin.
GN XLK15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987;
RA Olsson A.Y.; Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus".
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY152434; AAN78422.1; -.
DR MGD; MGI:2447533; K1k15.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_SIA.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 254 AA; 28042 MW; AA9E38BEBDD01861 CRC64;

Query Match 44.3%; Score 608; DB 11; Length 254;
Best Local Similarity 49.0%; Pred. No. 1e-50;
Matches 124; Conservative 30; Mismatches 77; Indels 22; Gaps 7;

QY 5 IFLLLCVGLSQAAT--PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
Db 1 MWLLAFVLIVSAAQDGVLEGEFCVPHSPQWQVALFERGNCAGFLISPRWVLTAAH 60

Qy	63	CSGGRYVRLGEHSLSQLDWTETQPHSGFSVTHPGYLCASTSHEDLLRLRLPVRVTS	122
Db	61	QCTRFMRVRLGEHNLRLKFDGPEQLRSVSRITPHPGY--EARTHREDIIMLLRLFKCARLTA	118
Qy	123	SVQPLPLPNDCATAGTECHVSGWGTTNPRNP-----FPDLLOCLNLSVSHAT	171
Db	119	YVRVALPRRCPPLIGEDCCVSGWGLLS--DNNPGATGSKSHVRLPDTLFCANISIISEAS	177
Qy	172	CHGYVPGRIITSNMVCA---GGVPGQDACQDSSGGPLVCGVLQGVISWGSVPCQGDGIP	228
Db	178	CNKDYPGRVLFTWCAGVEGG--GTDSCEDSSGGPLVCGEALQGVISWGDV-PCDTTITKP	234
Qy	229	GVYTYICKYVDWI	241
Db	235	GVYTKVCSYLEWI	247

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RESULT 4
ID QBIXD7
ID QBIXD7 PRELIMINARY; PRT; 275 AA.
AC QBIXD7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Variant form hippostasin/KLK11.
GN KLK11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Prostate;
RA Nakamura T., Miteui S., Miki T., Yamaguchi N.;
RT "Molecular cloning and expression of a variant form of
RT hippostasin/KLK11 in prostate.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB078780; BAC54105.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SP; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 275 AA; 30165 NW; 257A42B28F40E2C4 CRC64;

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Qy	215	SWGSVGPCGGDGPVGVYTYICKYVDWIRMWRNN	248
Db	243	SWGQ-DPCATRKPGVYTKVCKYVDWQETMKN	275
RESULT 5			
Q9QYN4			
ID	Q9QYN4	PRELIMINARY;	PRT; 249 AA.
DT	01-MAY-2000	(TrEMBLrel. 13, Created)	
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Hippostasin.		
GN	PRSS20.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
NCBI	NCBI_TaxID=10090;		
RX	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Yamaguchi N., Mitsui S.;		
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
[2]			
RC	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Mitsui S., Yamaguchi N.;		
RT	"CDNA cloning of a novel brain serine protease, Hippostasin.";		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB016226; BAA8825.1; -.		
DR	HSP; P00763; IDPO.		
DR	MEROPS; S01.257; -.		
DR	MGD; MGI:1929977; Prsa20.		
DR	GO; GO:0005576; C.extracellular; IDA.		
DR	InterPro; IPR009003; Cys_Ser_trypsin.		
DR	InterPro; IPR001254; Peptidase_S1.		
DR	InterPro; IPR001314; Peptidase_S1A.		
DR	Pfam; PF00089; trypsin; 1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	SMART; SM00020; Tryp_SPC; 1.		
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.		
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.		
DR	PROSITE; PS00135; TRYPSIN_SER; 1.		
SQ	SEQUENCE 249 AA; 27604 MW; F9FF9CB45D727D5 CRC64;		
	Query Match 43.5%; Score 597.5; DB 11; Length 249;		
	Best Local Similarity 47.0%; Pred. No. 1.1e-49;		
	Matches 118; Conservative 33; Mismatches 95; Indels 5; Gaps 4;		
Qy	1	MGLSIFLLCVLGSQAATPKINFTGTCGRNSQPWQVLFGFTGSLRCGGVLIDHRWLTA	60
Db	1	MILRLTALAVTGHVGGET-RIINGXYECRPHSQPQWALFQKTRLLCGATLIAPKWLTA	59
Qy	61	AKSGSRWYVRLGSHLSQLDWTQEIHRSGFVTHPGYLGA--STSEHDLRLRLPLV	118
Db	60	AKCKPHYVILGHNLEKTDGCEQRMAATESPHDPFNNSLPNKDRNDMLVKMSPV	119
Qy	119	RVTSVQPLPLPNDCATAGTECHVSGWGIITNHPRNPFDFLLQCLNLSIVSHATCHGVYPG	178
Db	120	FFTRAVQPLTLSPHCVAAGTSCILISGWTGTTSPQLRLPHSLRCANVSIIEHKECEKAYPG	179
Qy	179	RIITSNMYCAG-GVPGQACOGDGGPLVCGGVLOGLYSWGSVGPCGODGIPGVYTYCKY	237
Db	180	NIITDTMLCAVRKEGKDSQCGDGGPLVNCGSIQGIISWGQ-DPCAVTRKPGVYTKVCKY	238
Qy	238	VDWIRMIRNN 248	
Db	239	FNWIEVWRNN 249	
RESULT 6			
Q9QYN3			
ID	Q9QYN3	PRELIMINARY;	PRT; 276 AA.

Takayama T.K., Carter C.A., Deng T.;
"Activation of prostate-specific antigen precursor (pro-PSA) by
RT prostin, a novel human prostatic serine protease identified by
degenerate PCR.";
RL Biochemistry 40:1679-1687(2001).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AF303046; AAK62813.1; --
DR HSPSP; P00761.1ANL.
DR MEROPS; S01.081; --
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004235; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR003003; Cys Ser trypsin.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp SPc; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR Hydrolase; Protease; Serine protease.
KW SEQUENCE 255 AA; 27986 MW; 00D5B79E14B9468F CRC64;
Query Match 43.3%; Score 595; DB 4; Length 255;
Best Local Similarity 46.5%; Pred. No. 1.9e-49;
Matches 119; Conservative 32; Mismatches 87; Indels 18; Gaps 6
Qy 8 LLCVLGSLQAAT----PKIFNGTEGRNSQPQVGLFGTSLRCGGVLIHRHWLTAAHC 63
Dd 3 LLLTLISFLLSAQDGDKLLEGDECAPHSQPQVALYERGFNCGASLISPHWVLSAAHC 62
Qy 64 SGSRVYWRVLRGHSLSDLTWTQIRHSGFSVTHPGVIGASTSHEHDRLRLRLRPVRTSS 123
Dd 63 QSRFWRVLRGEHLKRDGPQLATTSTRVIPHPY--EARSHRNDIMLLRLVQPARINPQ 120
Qy 124 VQPIPLPNDCATAGTECHVSQGWGINH-----PRN--PPDDLQCLNTLSIVSHATCH 173
Dd 121 VRPAVLPTCRPHPGACVVGSGVLVSHNEPGTAGSPRSQVSLPDTLHCANIGIISDTSKD 180
Qy 174 GVYPGRITSNMVCAGGV-PGODACGDSGGPLVCGVLOGLVWSGVGPCQGDIHPGYVT 232
Dd 181 KSYPERLNTNMVVCAGEARGEGSCGDSGGPLVCGVLOGLVWSGDV-PCDNTTKPGYVT 239
Qy 233 YICKYVDWMIRMNN 248
Dd 240 KVCHYLEWIRETMKN 255
RESULT 8
ID Q9D140 PRELIMINARY; PRT; 293 AA.
AC Q9D140;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110030019rik protein.
GN 1110030019RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner T., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glssi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,

DR	MGD; MGI:2447564; Kklk14.
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.
DR	GO; GO:0004295; F:trypsin activity; IEA.
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR	InterPro; IPR009003; Cys Ser trypsin.
DR	InterPro; IPR001254; Peptidase_S1.
DR	InterPro; IPR001314; Peptidase_S1A.
DR	Pfam; PF00089; trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	SMART; SM00020; Tryp_SPC; 1.
DR	PROSITE; PS0240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
DR	SEQUENCE 250 AA; 27016 MW; F62FEBF2290FEBE8 CRC64;
SQ	
Query Match	42.6%; Score 586; DB 11; Length 250;
Best Local Similarity	47.2%; Pred. No. 1.4e-48;
Matches 120; Conservative 40; Mismatches 80; Indels 14; Gaps 7;	
Qy	5 IFLLLCVL-----GLSQ-AATPKIFNGTECGRNSQPWCVLFGTSLR--CGGVLIDHRW 56
Dd	1 MFLLLIIQLALVAIAQQSDHKIIGYRCVRNSQPWQVALAQPGHRTLCGGVLLSDQW 60
Qy	57 VLTAAHCSSGRYVWRIGEHSLSOLDWTQEIRHSGFSVTHPGYLCASTSHEDLRLLRL 116
Dd	61 VLTAAHCARPLNHALVKGNIRWEATQQVVARQVHPQY--QPQAHDNDLMLLKLOK 118
Qy	117 PVRTSSVQPLPDPNCATAGTCHTSVGWITNHPFPDILLOCLNLSTIVSHATGHVY 176
Dd	119 KVRLGRAVKTTISVASSCASPGTPCRVSGWGTTASPIARYPTALTQCNVNMISEQACHRAY 178
Qy	177 PGRITSNNVCAGVP--GODACOGDSGGPLVCCGVQLGVSWGSVGPCQGDLPGVVTYI 234
Dd	179 PGIIITGMVCA-GVPEGRKDCQDGSGGPLVCCGQLQELINSWG-MERCAMEGYEGVYANL 236
Qy	235 CKTVDMIRMIMRN 248
Dd	237 CNYHSMIQRTMQSN 250
RESULT 11	
Q80VS4	PRELIMINARY; PRT; 242 AA.
AC	Q80VS4;
DT	01-JUN-2003 (TrEMBLrel. 24, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Similar to kallikrein 14 (Fragment).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NWI; TISSUE=Breast tumor;
RA	Strauberg R.;
RL	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC047566; AAK4756.1; -
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.
DR	GO; GO:0004295; F:trypsin activity; IEA.
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR	InterPro; IPR009003; Cys Ser trypsin.
DR	InterPro; IPR001254; Peptidase_S1.
DR	InterPro; IPR001314; Peptidase_S1A.
DR	Pfam; PF00089; trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	SMART; SM00020; Tryp_SPC; 1.
DR	PROSITE; PS0240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
DR	NON TER
FT	1
SQ	SEQUENCE 242 AA; 26059 MW; A3F8A624DE481D36 CRC64;

Query Match 42.1%; Score 578; DB 11; Length 242;
Best Local Similarity 49.1%; Pred. No. 7.9e-48;
Matches 114; Conservative 35; Mismatches 75; Indels 8; Gaps 5;

QY 21 KIFNGTECGRNQPMQVGLFEGTSLR--CGVLIDHRWLTAHCGSGRYWRLGHSLS 78
DB 15 KLIIGYRCVRNQPQVLAQPGHFLPGVLLSDQWITAAHCAPIILHVALGXENR 74
QY 79 QLDWTEQIRHSGFSTHYPGYLGASTSHEHDLRLRLRPVTVSSVOPLEPNDCAATG 138
DB 75 RWEATQVVRVARQVHPQY--QPQAHNDMLLKLQKVKRLGRAVKTISVASSCASPT 132
QY 139 ECHVSGWGTINPRNPPDLLOCLNLSIVSHATCHGVYQGRITSNNVACAGVP--QDQAC 196
DB 133 PCRVSGWGTIATPIAKYPTALQCVNINMSEQACHRAYPGIITSVGMVCA-GVPEGKDC 191
QY 197 QDSDGGLVCGVLOGLVSWGSGVPCGQDIPGVYVYICKYVDWIRMNRN 248
DB 192 QDSDGGLVCGVLOGLVSWG-MERCAMPYPGVYANLCNHYSHWIRTQSN 242

RESULT 12

Q7SZT1 PRELIMINARY; PRT; 248 AA.

AC Q7SZT1; 248 AA. 248 AA.
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Trypsin (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Klein S., Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056068; AAH56068.1; -.

FT NON_TER 1 1
SQ SEQUENCE 248 AA; 26494 MW; 1ED9D0D218702860 CRC64;

Query Match 41.0%; Score 563; DB 13; Length 248;
Best Local Similarity 45.0%; Pred. No. 2.3e-46;
Matches 112; Conservative 46; Mismatches 83; Indels 8; Gaps 5;

QY 3 LSIFLLCVLGLSQA--ATPKIFNGTECGRNQPMQVGLFEGTSLRCCGVLDHRWLTA 60
DB 5 MKFLVILLGAAVAFEDDDDKIVGGFTCAKNAPVQVSLNAGYHF-CGGSLSINQWVSA 63
QY 61 AHCSGSRYWRLGHSLSOLDWTEQIRHSGFSTHYPGYLGASTSHEHDLRLRLRPVTV 120
DB 64 AHCYSRIQVRGHEHIALNEGTEQIDSKVKEPNY--NSRLNDMLIKLSTARL 121
QY 121 TSSVQPLPLPNDCAATAGTECHVSGMGTINPRNPPDLLOCLNLSIVSHATCHGVYVPGRI 180
DB 122 SANIQSVLPFSACASAGTNCILISGWTNLTSSGTNYPDLLQCLNAPILTDSQNSYPGEI 181
QY 181 TSNVWCAGVP-QDQACQDSDGGLVCGVLOGLVSWGSGVPCGQDIPGVYVYICKYVD 239
DB 182 TKNMFCAGFLAGKDCQDSDGSGPVVVCNGQLQGVSWGY--GCAQRNYPGVYVYCKNFVT 239
QY 240 WIRMNRN 248
DB 240 WQSTISSN 248

RESULT 13

Q7SZ06 PRELIMINARY; PRT; 243 AA.

AC Q7SZ06; 243 AA. 243 AA.
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Klein S., Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056068; AAH56068.1; -.

```

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054194; AA054194.1; -.
KW Hypothetical protein.
SQ SEQUENCE 243 AA; 25476 MW; C5B82B458B209F31 CRC64;

Query Match 40.4%; Score 555; DB 13; Length 243;
Best Local Similarity 45.7%; Pred. No. 1.3e-45;
Matches 113; Conservative 42; Mismatches 82; Indels 10; Gaps 6;

Qy 6 FLLLCVGLGSOAAT---PKIPNGTECGRNSQPMQVGLFEGTSRLCGGLVIDHRLWLTAAH 62
Db 3 FLLLCVGLGSOAAT---PKIPNGTECGRNSQPMQVGLFEGTSRLCGGLVIDHRLWLTAAH 60
Qy 63 CSGRYVWRLGHSLSQDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTS 122
Db 61 CYKASIQVRLGHEHIALSEGTEQFISSKVIHSGY--NSYLDNDIMLKLSFASINA 118
Qy 123 SVQPLPLPNDCATAGTECHVSGWGITNHPNPFDDLLQCLNLSIVSHATGCHGVYPRITS 182
Db 119 AVNTVPLPSCSAAGTCLISGWGNTLSNGSNYPDLLQCLNAPILTNACQNSAYPGEITA 178
Qy 183 NMVCAGGVPGQACQDGGPLVCGGLVQLGSLVSGVPGCGQDGIQGVYTYICKYVDWI 241
Db 179 NMICVGFMEGKDCQDGGPVCNGQLQGVVSGY--GCAMENYFGVYTKVCYNNAWI 236
Qy 242 RMIMRN 248
Db 237 QNTIAAN 243

RESULT 14
O88301 PRELIMINARY; PRT; 246 AA.
AC O88301, 1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine protease (BSP).
GN PRSS18 OR MBSP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Matsui H., Takahashi T.;
RA Meier N., Dear T.N., Boehm T.;
RT "A novel serine protease preferentially expressed in brain.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Skin;
RA Meier N., Dear T.N., Boehm T.;
RT "Mouse serine protease preferentially expressed in brain.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Mateui H., Takahashi T.;
RT "The sequences of mouse serine protease gene expressed in brain.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB015206; BAA28895.1; -.
DR EMBL; Y18723; CAA77269.1; -.
DR EMBL; AB032402; BAA84544.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.236; -.
DR MGD; MGI:1343166; Prss18.

GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
PFam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYP SIN DOM; 1.
DR PROSITE; PS00134; TRYP SIN HIS; 1.
DR PROSITE; PS00135; TRYP SIN SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 246 AA; 27496 MW; E20C080087139B63 CRC64;

Query Match 40.3%; Score 553.5; DB 11; Length 246;
Best Local Similarity 43.5%; Pred. No. 1.9e-45;
Matches 107; Conservative 46; Mismatches 82; Indels 11; Gaps 6;

Qy 7 LLLCVGLGSOAA---TPKIPNGTECGRNSQPMQVGLFEGTSRLCGGLVIDHRLWLTAAH 62
Db 4 LALLCVL-LAKSAWSEBQEKVHGGPCLDKSHFPQAALYTSGLLCGGLVIDPQWLTAAH 62
Qy 63 CSGRYVWRLGHSLSQDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTS 122
Db 63 CKPKNQVLIGKXNLKQTETFORQISVDRIIVPRY--NPETHNDIMVHLKXNPVKFSK 120
Qy 123 SVQPLPLPNDCATAGTECHVSGWGITNHPNPFDDLLQCLNLSIVSHATGCHGVYPRITS 182
Db 121 KIQPLPLKNDCEENPNCILGWG--KMENGDFDTIQCADVHLVPREQERAYPGKITQ 178
Qy 183 NMVCAGGVPGQACQDGGPLVCGGLVQLGSLVSGVPGCGQDGIQGVYTYICKYVDWI 241
Db 179 SMVCGADMKEGNDSCQDGGPLVCGGLRGLVSGWDM-PCGSKBKPQGVYTDVCTHIRWI 237
Qy 242 RMIMRN 247
Db 238 QNTIRN 243

RESULT 15
Q91Y82 PRELIMINARY; PRT; 253 AA.
AC Q91Y82, 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neurosin (Protease, serine, 18).
GN PRSS18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Matsui S., Yamaguchi N.;
RT "cDNA cloning and characterization of mouse brain specific serine
protease, Neurosin.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB008928; BAB55605.1; -.
DR EMBL; BC031119; AAH31119.1; -.
DR HSSP; P00761; LAN1.
DR MEROPS; S01.236; -.
DR MGD; MGI:1343166; Prss18.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.

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OM protein - protein search, using sw model

Run on: June 15, 2004, 16:11:51 ; Search time 17 Seconds
(without alignments)
759.612 Million cell updates/sec

Title: US-10-006-856A-194
Perfect score: 1374
Sequence: 1 MGLSIFLLLCVLGLSQARP.....GVYTYICKYVDIMRMNN 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1374	100.0	248	1	KLK8 HUMAN
2	630.5	45.9	260	1	KLK8 HUMAN
3	621.5	45.3	260	1	NRPN MOUSE
4	621.5	45.2	260	1	NRPN RAT
5	618.5	45.0	280	1	KLK8 HUMAN
6	599	43.6	256	1	KLK8 HUMAN
7	569.5	41.4	248	1	TRY3 CHICK
8	569.5	41.4	251	1	KLK8 HUMAN
9	568.5	41.4	250	1	KLK9 HUMAN
10	567	41.3	277	1	KLK8 HUMAN
11	566	41.2	248	1	TRY2 CHICK
12	565	41.1	248	1	TRY1 CHICK
13	564.5	41.1	293	1	KLK5 HUMAN
14	564	41.0	276	1	KLK4 HUMAN
15	563	41.0	244	1	TRY2 XENLA
16	561	40.8	231	1	TRYP PIG
17	561	40.8	243	1	TRY1 BOVIN
18	561	40.8	244	1	KLK6 HUMAN
19	555	40.4	243	1	TRY1 XENLA
20	555	40.4	253	1	KLK7 HUMAN
21	553	40.2	246	1	TRY2 MOUSE
22	550	40.0	247	1	TRY2 BOVIN
23	546	39.7	247	1	TRY2 CANFA
24	545	39.7	246	1	TRY1 CANFA
25	544.5	39.6	247	1	TRY3 RAT
26	543	39.5	246	1	TRY1 RAT
27	540	39.3	238	1	TRY3 SALSA
28	533.5	38.8	247	1	TRY4 RAT
29	533	38.8	246	1	TRY2 RAT
30	527.5	38.4	261	1	KLK7 RAT
31	521.5	38.0	246	1	KLK_FIG
32	521.5	38.0	261	1	KLK6 MOUSE
33	519	37.8	246	1	TRYA RAT

ALIGNMENTS

RESULT 1

ID	KLKC HUMAN	STANDARD;	PRT;	248 AA.
AC	Q9UKR0; Q9UKR1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Kallikrein 12 precursor (BC 3.4.21.-) (Kallikrein-like protein 5)			
DE	(KLK-L5).			
GN	KLK12 OR KLK15.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	MEDLINE=20118156; PubMed=10652563;			
RA	Yousef G.M., Luo L.-Y., Diamandis E.P.;			
RT	"Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4.";			
RT	Anticancer Res. 19:2843-2852(1999).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;			
RT	"Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLK-L5).";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	MEDLINE=20510030; PubMed=11054574;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,			
RA	Moss P., Paepel B., Wang K.;			
RT	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";			
RL	Gene 257:119-130(2000).			
RL	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RA	Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,			
RA	Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,			
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J.,			
RA	Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,			
RA	Andreise T., Frankheim M., Attix C., Amico-keller G., Coefield J.,			
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,			
RA	Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,			
RA	Olsen A.S., Carrano A.V.;			
RT	"Sequence analysis of chromosome 19q13.4.";			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: Secreted (Probable).			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	Isold=Q9UKR0-1; Sequence=Displayed;			
CC	Name=2;			
CC	Isold=Q9UKR0-2; Sequence=VSP_005403;			
CC	-1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.			

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CC -----
 CC EMBL; AF135025; AAD26426.2; -;
 CC EMBL; AF135025; AAF06065.1; -;
 CC EMBL; AF243527; AAG33365.1; -;
 CC EMBL; AC011473; AAG23258.1; -;
 CC HSSP; P00763; LDPO.
 CC MEROPS; S01.020; -;
 CC Genew; HGNC:6360; KKL12.
 CC MIN; 605539; -;
 CC GO; GO:000576; C:extracellular; NAS.
 CC GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
 CC GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00020; TRYD_SPC; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Hydrolase; Serine protease; Glycoprotein; Signal;
 CC Alternative splicing.
 CC SIGNAL 1 17
 CC CHAIN 18 248
 CC KALLIKREIN 12.
 CC ACT_SITE 62 62
 CC CHARGE_RELAY_SYSTEM (BY SIMILARITY).
 CC ACT_SITE 108 108
 CC CHARGE_RELAY_SYSTEM (BY SIMILARITY).
 CC ACT_SITE 200 200
 CC CHARGE_RELAY_SYSTEM (BY SIMILARITY).
 CC BY SIMILARITY.
 CC DISULFID 28 161
 CC BY SIMILARITY.
 CC DISULFID 47 63
 CC BY SIMILARITY.
 CC DISULFID 133 235
 CC BY SIMILARITY.
 CC DISULFID 140 206
 CC BY SIMILARITY.
 CC DISULFID 172 186
 CC BY SIMILARITY.
 CC DISULFID 196 222
 CC BY SIMILARITY.
 CC CARBOHYD 24 24
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 163 163
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC KVDWIRMIMNKN -> NSTLVGLGTSWNFNSQPF (in
 CC isoform 2).
 CC /FTid-VSP 005403.
 CC SEQUENCE 248 AA; 26733 MW; B8473E98F8BAP703 CRC64;
 CC
 CC Query Match 100.0%; Score 1374; DB 1; Length 248;
 CC Best Local Similarity 100.0%; Pred. No. 1.7e-105;
 CC Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 MGLSIFLLCVLGLSQATPKLFGTEGRNSQPMQVGLFGTSLRCGVLIDHRWLTA 60
 CC DB 1 MGLSIFLLCVLGLSQATPKLFGTEGRNSQPMQVGLFGTSLRCGVLIDHRWLTA 60
 CC
 CC QY 61 AHCSSRSYVWVRLGSHLSQLDWTQIRHSGFVSVTHPGYLGASTSHEHDLRLRLPVRV 120
 CC DB 61 AHCSSRSYVWVRLGSHLSQLDWTQIRHSGFVSVTHPGYLGASTSHEHDLRLRLPVRV 120
 CC
 CC QY 121 TSSVQPLPLNDACATAGTECHVSGMGITNHPNPPDILQCLNLSIVSHATCHGVYVPGRI 180
 CC DB 121 TSSVQPLPLNDACATAGTECHVSGMGITNHPNPPDILQCLNLSIVSHATCHGVYVPGRI 180
 CC
 CC QY 191 TSNMVCAGVPGQACQDSGGPLVCGVGLQSLVSGVSGPCQDGPVVTYICKYVDW 240
 CC DB 191 TSNMVCAGVPGQACQDSGGPLVCGVGLQSLVSGVSGPCQDGPVVTYICKYVDW 240
 CC
 CC QY 241 IRMIMRNN 248
 CC DB 241 IRMIMRNN 248

RESULT 2
 KKL8 HUMAN STANDARD; PRT; 260 AA.
 ID AC O60259; Q9HCB3; Q9U1L9; Q9UQ47;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neuropepsin precursor (BC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine
 DE protease TADG-14) (Tumor-associated differentially expressed gene-14
 DE protein).
 DE KKL8 OR PRSS19 OR TADG14 OR NRPN.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hippocampus;
 RX MEDLINE=98372070; PubMed=9714609;
 RA Yoshida S., Taniguchi M., Hirata A., Shiozaka S.;
 RT "Sequence analysis and expression of human neuropepsin cDNA and gene.";
 RL Gene 213:9-16 (1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=99203457; PubMed=10102990;
 RA Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
 RT "A novel form of human neuropepsin, a brain-related serine protease, is
 RT generated by alternative splicing and is expressed preferentially in
 RT human adult brain.";
 RL Eur. J. Biochem. 260:627-634 (1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Ovary;
 RX MEDLINE=99413504; PubMed=10485494;
 RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Farnley T.H.,
 RA O'Brien T.J.;
 RT "Cloning of tumor-associated differentially expressed gene-14, a novel
 RT serine protease overexpressed by ovarian carcinoma.";
 RL Cancer Res. 59:4435-4439 (1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC Gan L., Gellinas R., Gown A.M., Moss P., Smith R., Wang K.;
 RT "Molecular cloning and characterization of a novel serine protease,
 RT ovasin, a potential molecular marker for ovarian carcinomas.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepel B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130 (2000).
 RN [6]
 RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).
 RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
 RA Danganan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of chromosome 19q13.4.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Suggested to be involved in kindling epileptogenesis and
 CC hippocampal plasticity.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;

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CC      IsoId=O60259-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=O60259-2; Sequence=VSP_005401;
CC      TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in the
CC      pancreas while isoform 2 is expressed in adult brain and
CC      hippocampus. Both forms are also found in fetal brain and
CC      placenta. Not detected in kidney, spleen, liver and lung.
CC      -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AB009849; BAA28673.1; -
CC      EMBL; AB012761; BAA28676.1; -
CC      EMBL; AB010780; BAA88684.1; -
CC      EMBL; AB008390; BAA82665.1; -
CC      EMBL; AB008927; BAA82666.1; -
CC      EMBL; AF055982; AAD56050.1; -
CC      EMBL; AF095742; AAD25979.1; -
CC      EMBL; AF095743; AAD29574.1; -
CC      EMBL; AF243527; AAG33361.1; -
CC      EMBL; AC011473; AAG23254.1; -
CC      HSSP; Q61955; INPM.
CC      MEROPS; S01.244; -.
CC      Genew; HGNC:6369; KLK8.
CC      MIM; 605644; -.
CC      GO; GO:0008236; F-serine-type peptidase activity; TAS.
CC      GO; GO:0007399; P-neurogenesis; TAS.
CC      GO; GO:0007399; P-neurogenesis; TAS.
CC      InterPro; IPR009003; Cys Ser trypsin.
CC      InterPro; IPR001254; Peptidase S1.
CC      InterPro; IPR001314; Peptidase_S1A.
CC      Pfam; PF00089; trypsin; 1.
CC      PRINTS; PR00722; CHYMOTRYPSIN.
CC      SMART; SM00020; Tryp_SPC; 1.
CC      PROSITE; PS00240; TRYPSIN_DOM; 1.
CC      PROSITE; PS00134; TRYPSIN_HIS; 1.
CC      PROSITE; PS00135; TRYPSIN_SER; 1.
CC      KW Hydrolyase; Serine protease; Glycoprotein; Zymogen; signal;
CC      alternative splicing.
CC      SIGNAL 1 28 POTENTIAL.
CC      PROPEP 29 32 BY SIMILARITY.
CC      CHAIN 33 260 NEUROPSIN.
CC      ACT_SITE 73 73 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC      ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC      ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC      DISULFID 39 173 BY SIMILARITY.
CC      DISULFID 58 74 BY SIMILARITY.
CC      DISULFID 145 246 BY SIMILARITY.
CC      DISULFID 152 218 BY SIMILARITY.
CC      DISULFID 184 198 BY SIMILARITY.
CC      DISULFID 208 233 BY SIMILARITY.
CC      CARBOHYD 110 110 N-LINKED (GLCNAC... ) (POTENTIAL).
CC      VARSPLIC 23 23 A -> AACGSLDLTKLYAENLPCVHLNWPQSPHCPGRG
CC      WRNPLPPA (in isoform 2).
CC      /FTID=VSP_005401.
CC      SEQUENCE 260 AA; 28048 MW; EF439E5B8C83E660 CRC64;
CC      Query Match 45.9%; Score 630.5; DB 1; Length 260;
CC      Best Local Similarity 50.2%; Pred. No. 1.1e-44;
CC      Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;
CC      5 IFLLI---CVLGLSQAATPKIFNGTEGRNSQPMQVGLFEGTSLRCGVLIDHRWLTAA 61
CC      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC      13 MFLLLGGAWAGHSRAQEDKVLGCGECQPHSQPMQAALFQQLQCGVLVGGNWLTA 72
CC      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC      62 HCSGRYRWRLGHSLSQLDWTQIRISGFSVTHPGVLGAST-SHEHDLRLRLRPVR 120
CC      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC      73 HCKPKYTVRLGHSLSQNDGPEQEIFVQSIHPHCYNSSDVEDHNDHMLQLRDAQSL 132

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QY 121 TSSVOPLPDPNDCATAGTECHVSGWGIYTHNPRNPFDDLLQCLNLSIVSHATCHGVYPGRI 180
DB 133 GSKVAFISLADHCTQPGKCTVTKTSPRENFDTLNCBAEVKIFPKKCEDAYPGOI 192
QY 181 TSNMYCAGVPGQDACQGDGSGPLVCGVQLQVSWGSGVPGQDGIQGVYIYIKYVDW 240
DB 193 TDCMVCASSKKGADTCQGDGSGPLVCDGALQGITWGS-DPCGRSDKPGVYINI CRYLDM 251
QY 241 IRMIM 245
DB 252 INKII 256
RESULT 3
NRPN MOUSE STANDARD; PRT; 260 AA.
ID NRPN MOUSE STANDARD; PRT; 260 AA.
AC Q61955;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neopsin precursor (SC 3.4.21.-) (NP) (Kallikrein 8).
GN KLK8 OR PRSS19 OR NRPN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hippocampus;
RX MEDLINE=95348817; PubMed=7623137;
RA Chen Z.-J., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
RA Ito J., Nishino H., Aimoto S., Kiyama H., Shiozaka S.;
RT "Expression and activity-dependent changes of a novel limbic-serine
RL J. Neurosci. 15:5088-5097(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Yoshida S., Hirata A., Inoue N., Shiozaka S.;
RT "Cloning and assignment of mouse neuropsin gene, Prss19 to chromosome
RL 7B4."
RN [3]
RP Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=98225202; PubMed=9556608;
RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
RA Shiozaka T., Madorikawa R., Kamachi T., Kawabe A., Shiozaka S.;
RT "Characterization of recombinant and brain neuropsin, a

```


RP SEQUENCE FROM N.A.
RC STRAIN=Fischer; TISSUE=Brain;
RX MEDLINE=9838725; PubMed=9722524;
RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
RT "Serine proteases in rodent hippocampus";
RL J. Biol. Chem. 273:23004-23011(1998).
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity. Has a strong proteolytic activity against
CC fibronectin (By similarity).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Restricted to hippocampus.
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC
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CC
CC EMBL: AJ005641; CAA06643.1; -
DR HSRP; Q61955; INPM.
DR MEROPS; S01.244; -
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SRR; 1.
KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 28 POTENTIAL.
FT PROPEP 29 32 BY SIMILARITY.
FT CHAIN 33 260 NEUROPSIN.
FT ACT_SITE 73 73 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 39 173 BY SIMILARITY.
FT DISULFID 58 74 BY SIMILARITY.
FT DISULFID 145 246 BY SIMILARITY.
FT DISULFID 152 218 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 208 233 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A0B7F5 CRC64;
Query Match 45.2%; Score 621.5; DB 1; Length 260;
Best Local Similarity 48.6%; Pred. No. 6.1e-44;
Matches 118; Conservative 32; Mismatches 90; Indels 3; Gaps 3;
QY 5 IFLL-CVTLGSAATPKLFGNTECGRNSOPQVGLFEGTSLRCGGVLIDRWLTAHC 63
Db 15 LFLMGAGAGLTAQSKILEGQCKPHSQPQWTFALFQGRVLCGGVLGDRWLTAHC 74
QY 64 SGSRVYVRLGHSLSQDWTQEIQRHSGFSVTHPGYLGAS-TSEHDLRLRLRLPVRVTS 122
Db 75 KDKYSVRLGDHSLQKDEFEQETQVARSIQHPCFNSSNPEDSHDMLRLQNSANLGD 134
QY 123 SVQPLPLPNDCATAGTECHVSGWGTNHPNPPDQLQCLNLSIVSHATGCHVPGRITS 182
Db 135 KVXPIELANLCPKVGQRCKIISGWGTVTSPQENFNTLCAEVKISQNKCEAYPPGKITE 194
QY 183 NMVCGGVPGDACCQGGSGGLVCGGVGLQGVSVGPGQDGPVGVYVYICKYVDWIR 242
Db 195 GMVCGAGSGNADTCQGSQGGPLVCGVGLQGLTGWGSDPCCKPKPGVYICKRYTNWIK 253
QY 243 MIM 245

Db 254 KTM 256
RESULT 5
KLKB HUMAN STANDARD; PRT; 250 AA.
ID Q9UBX7; O75837; Q9NSG5;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Kallikrein 11 precursor (EC 3.4.21.-) (Hippostasin) (Trypsin-like
DE protease)
GN KLK11 OR PRSS20 OR TLSP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hippocampus;
RX MEDLINE=98438738; PubMed=9765601;
RA Yoshida S., Taniuchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;
RT "cDNA cloning and expression of a novel serine protease, TLSP";
RL Biochim. Biophys. Acta 1399:225-228(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Hippocampus, and Prostate;
RX MEDLINE=20329229; PubMed=10872828;
RA Mitui S., Yamada T., Okui A., Kominami K., Uemura H., Yanaguchi N.;
RT "A novel isoform of a kallikrein-like protease, TLSP/hippocastin,
RT (PRSS20), is expressed in the human brain and prostate.";
RL Biochem. Biophys. Res. Commun. 272:205-211(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20130117; PubMed=10662548;
RA Yousef G.M., Scorilas A., Diamandis E.P.;
RT "Genomic organization, mapping, tissue expression, and hormonal
RT regulation of trypsin-like serine protease (TLSP PRSS20), a new
RT member of the human kallikrein gene family.";
RL Genomics 63:88-96(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci R.D., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blackley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Green E.D., Dickson M.C.,
RA Butterfield V.S.N., Kryzysinski M.I., Skalska U., Smalus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Possible multifunctional protease. Efficiently cleaves
CC bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and
CC weakly cleaves other substrates for kallikrein and trypsin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UBX7-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UBX7-2; Sequence=VSP_005402;
CC -!- TISSUE SPECIFICITY: Expressed in brain, skin and prostate. Isoform
CC 1 is expressed preferentially in brain; isoform 2 in prostate.
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC -----
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CC -----
DR EMBL; AB012917; BAA33404.1; ALT_INIT.
DR EMBL; AB013730; BAA88713.1; -.
DR EMBL; AB041036; BAA36797.1; -.
DR EMBL; AF164623; AAD47815.1; -.
DR EMBL; AF243527; AAG33364.1; -.
DR EMBL; AC011473; AAG33257.1; -.
DR EMBL; BC022068; AAB22068.1; -.
DR HSPB; P00763; LDPO.
DR MEROPS; S01.257; -.
DR Genew; HGNC:6359; KLUK11.
DR MIM; 604434; -.
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;
KW Alternative splicing.
FT SIGNAL 1 18
FT PROPEP 19 21
FT CHAIN 22 250
FT KALLIKREIN 11.
FT ACT_SITE 62 62
FT ACT_SITE 110 110
FT ACT_SITE 203 203
FT DISULFID 28 163
FT DISULFID 47 63
FT DISULFID 135 237
FT DISULFID 142 209
FT DISULFID 174 188
FT DISULFID 199 224
FT DISULFID 99 99
FT CARBOHYD 165 165
FT CARBOHYD 181 181
FT CARBOHYD 210 210
FT VARSPPLIC 1 1
M -> MQLRLWLRDMKSSGRGLTAKEPGARSSPLQAM

FT (in isoform 2).
FT /FTId=VSP_005402.
SQ SEQUENCE 250 AA; 27466 MW; 192D910BECDC7A56 CRC64;
Query Match 45.0%; Score 618.5; DB 1; Length 250;
Best Local Similarity 48.2%; Pred. No. 1e-43;
Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;
Qy 3 LSTFLLCVLGLSOATPKIFNGTEGCRNSQPMQVGLFEGTSLRCGGVLIDHRLVLTAAH 62
Db 4 LQITLLALATGLVGGET-RIIKGFEPKSPQQAALFEKTRLLCGATLAPRWLLTAAH 62
Qy 63 CSGSRVYVRLGERSLSQDTEQIRHSGFVTHPGYLGA--STSHEHDLRLRLRPVRV 120
Db 63 CLKPRYIVHLQHNLOKRGCEQTRTATSFPHGFNNSLPNKDRNDIMLVKMASPVSI 122
Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGTINHPNRPFDLLQCLNLSIVSHATCHGVYVGR 180
Db 123 TWAVRPLTSSRCVTTAGTSCLLISGWGSTSPQLRPHTRLCANITITIEHOKENAYFGNI 182
Qy 181 TSNMVCAG-GVPGQDACGDSGGPLVCGVLQGLVSGSVGPGQDGIPIGVYTVICKYVD 239
Db 183 TDTMVCASVQGGKSCQGGSGGLVCNQLQGIISWGQ-DPCAITRPGVYTKVCKYVD 241
Qy 240 WIRMIMENN 248
Db 242 WIQETMKN 250
RESULT 6
KLUK1 HUMAN
ID_KLXF HUMAN STANDARD; PRT; 256 AA.
AC Q9H2R5; Q15358; Q9H2R3; Q9H2R4; Q9H2R6; Q9HBG9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).
GN KLUK15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RX PubMed=11010966;
RA Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;
RT "Molecular cloning of the human kallikrein 15 gene (KLUK15). Up-
RT regulation in prostate cancer.";
RL J. Biol. Chem. 276:53-61(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Faepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=94289486; PubMed=8018728;
RA Dhanich M.E., Spiess M.;
RT "A novel serine proteinase-like sequence from human brain.";
RL Biochim. Biophys. Acta 1218:225-228(1994).
CC -!- FUNCTION: Protease whose physiological substrate is not yet known.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q9H2R5-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9H2R5-2; Sequence=VSP_005405;
CC Name=3;


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Db 179 YPRTITPMVCA-GVPGGKDSQGDGGPLVCRQLQGLVSWG-MERCALPGYPGYTN 236
Qy 234 ICKYVDWIRMN 247
Db 237 LCKYRSWEETMRD 250

RESULT 9
KLK9 HUMAN
ID -KLK9 HUMAN STANDARD; PRT; 250 AA.
AC Q9UKQ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-
DE L3).
GN KLK9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13.3-q13.4.";
RL Anticancer Res. 19:2843-2852(1999).
RN [2]
RX MEDLINE=20247258; PubMed=10783266;
RA Yousef G.M., Diamandis E.P.;
RT "The expanded human kallikrein gene family: locus characterization and
RT molecular cloning of a new member, KLK-L3.";
RL Genomics 65:184-194(2000).
RN [3]
RX MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RX MEDLINE=20510030; PubMed=11054574;
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBAJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: Skin, thymus, trachea, cerebellum and spinal
CC cord.
CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC
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CC
CC EMBL; AF135026; AAD26427.2; -
CC EMBL; AF243527; AAG33362.1; -
CC EMBL; AC011473; AAG23255.1; -
CC HSSP; P00763; 1DPO.

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DR MEROPS, S01.307; -
DR Genew; HGNC:6370; KLK9.
DR MIM; 605504; -
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys_Ser_cysteine.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 15
FT CHAIN 16 250
FT ACT_SITE 63 63
FT ACT_SITE 111 111
FT ACT_SITE 204 204
FT DISULFID 29 164
FT DISULFID 48 64
FT DISULFID 136 238
FT DISULFID 143 210
FT DISULFID 175 189
FT DISULFID 200 225
FT CARBOHYD 131 131
FT CARBOHYD 166 166
FT CARBOHYD 211 211
SQ SEQUENCE 250 AA; 27512 MW; P2785245B063E98B CRC64;

Query Match 41.4%; Score 568.5; DB 1; Length 250;
Best Local Similarity 46.7%; Pred. No. 1.3e-39;
Matches 119; Conservative 32; Mismatches 89; Indels 15; Gaps 7;

Qy 1 MGLSIFLLCVGLSQATPKIFNGTEGRNSQVQWGLFEGSLRCGVLIDHRWLTA 60
Db 3 IGLLCALLSLAGHGWDT-RAIGAEERCRNSQVQWGLFHLTLFCATYLSIDRWLTA 61
Qy 61 AHCSGRYVRLGELSHLSQLDWTQIRHSGFSVT---HPGY---LGASTSHEDLRLR 113
Db 62 AHCKPKYVRLGELHLMKWEQPEQL---FRVTDFFPHFGNKLSAN-DHNDIMLIR 116
Qy 114 LRLPVRVTSSVQPLPLNDCATAGTECHVSGWGLTNPDPFPDGLLQCLMISVSHATCH 173
Db 117 LPRQARLSAPVQPLNLSQTCVSPQMQLISGWAQVSSPKALFPVTLQCANISILEKLCH 176
Qy 174 GVPYGRITSNMVCAG-GVPGQDACCQSDGGLVCGVQLGVLVSGVSGVPGQDQIPGYVT 232
Db 177 WAPYGHLSDSMLCAGLWEGRGSCQSDGGLVCGVQLGVLVSGVSGVPGQDQIPGYVT 235
Qy 233 YICKYVDWIRMN 247
Db 236 SVCHYDWIQEIMEN 250

RESULT 10
KLK9 HUMAN
ID -KLK9 HUMAN STANDARD; PRT; 277 AA.
AC Q9UKR3; Q9Y433;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)
DE (KLK-L4).
GN KLK13 OR KLKLA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=20229789; PubMed=10766816;
RA Yousef G.M., Chang A., Diamandis E.P.;
RT "Identification and characterization of KLK-L4, a new kallikrein-like
RN gene that appears to be down-regulated in breast cancer tissues.";
RL J. Biol. Chem. 275:11891-11898 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RA "Sequence analysis of chromosome 19q13.4.";
RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-180 FROM N.A.
RC TISSUE=Uterus;
RA Anasoge W., Winkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: Expressed in prostate, breast, testis and
CC salivary gland.
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC
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CC
CC EMBL; AF135024; AAC26425.2; -
CC EMBL; AC011473; AAC23259.1; -
CC EMBL; AL050220; CAB43320.1; ALT_INIT.
CC HSP; P00763; IDPO.
CC MEROPS; S01.306; -
CC Genew; HGNC:6361; KKL13.
CC MIM; 605505; -
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
CC GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS02040; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Serine protease; Glycoprotein; Signal.
CC SIGNAL 1 16
CC CHAIN 17 277
CC KALLIKREIN 13.
CC ACT SITE 76 76
CC CHARGE RELAY SYSTEM (BY SIMILARITY).
CC ACT SITE 124 124
CC CHARGE RELAY SYSTEM (BY SIMILARITY).
CC ACT SITE 218 218
CC CHARGE RELAY SYSTEM (BY SIMILARITY).
CC DISULFID 42 178
CC BY SIMILARITY.
CC DISULFID 61 77
CC BY SIMILARITY.
CC DISULFID 157 224
CC BY SIMILARITY.
CC DISULFID 189 203
CC BY SIMILARITY.
CC DISULFID 214 239
CC BY SIMILARITY.
CC CARBOHYD 30 30
CC N-LINKED (GLCNAC... ) (POTENTIAL).
CC CARBOHYD 225 225
CC N-LINKED (GLCNAC... ) (POTENTIAL).
CC CONFLICT 170 180
CC VNIPTKQCAN -> GMPHPWPEAP (IN REF. 3).
CC SEQUENCE 277 AA; 30570 MW; B8A9E8DCFB5D542 CRC64;
Query Match 41.3%; Score 567; DB 1; Length 277;
Best Local Similarity 46.8%; Pred. No. 1.9e-39;
Matches 116; Conservative 36; Mismatches 80; Indels 16; Gaps 6;

```

```

QY 13 GLSQATPKIFN-----GTECRNSQPHQVGLFEGTSIRCGVLIDHRWVLTAAH 62
DB 18 GVSQSS-KVINTNGTSGFLPGGYTCFPHSQPQAALLVQRLCCGVLVHPKWLTAH 76
QY 63 CSGRYWVRLSHGHSLSQLDWTEQIRHSGFSVTHPGVYGAST--SHEHDLRLRLRPVRV 120
DB 77 CLKEGLKYLKHALGRVEAGEQVREVTHSIPHPYRRSPTHLNHDDIMLLEQSPVQL 136
QY 121 TSSVQPLPLP-NDCAATAGTECHVSGMGTNHPRNPPFDLLQCLNLSIVSHATGHVYVGR 179
DB 137 TGVITQLPLSHNNRLTPGTTTCRVSGWGTTPSQVNYPKTKQCANIQLRSEDECKQVYVPGK 196
QY 180 ITSNMVCAGVGP-QDACAQSDSGPLVCGVGLQGLYSWGSVGCQGDIGPVVITYICKYV 238
DB 197 ITDNMLCAGTKEGGKDSCEGDSGGPLVNCNRTLYGIVSWGDF-FCGQPDPRFGVTVRSRYV 255
QY 239 DWIRMIWR 246
DB 256 LWIRETIR 263

RESULT 11
TRY2 CHICK
ID TRY2 CHICK STANDARD; PRT; 248 AA.
AC Q90628;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Trypsin I-P38 precursor (EC 3.4.21.4).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaea; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=95251611; PubMed=7733885;
RA Wang X., Gan L., Lee I., Hood L.E.;
RT "Isolation and characterization of the chicken trypsinogen gene
RT family.";
RL Biochem. J. 307:471-479 (1995).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: High levels are seen in the pancreas while
CC lower levels are found in the liver, spleen and thymus.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC
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CC
CC EMBL; U15156; AAA73913.1; -
CC PIR; S55067; S55067.
CC HSP; P00763; IDPO.
CC MEROPS; S01.258; -
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS02040; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Serine protease; Digestion; Pancreas; Zymogen;
CC Calcium-binding; Signal; Multigene family.
KW

```

FT SIGNAL 1 15 BY SIMILARITY.
 FT PROPEP 16 25 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 26 248 TRYPSIN I-P38.
 FT ACT SITE 65 65 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT METAL 77 77 CALCIUM (BY SIMILARITY).
 FT METAL 79 79 CALCIUM (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 87 87 CALCIUM (BY SIMILARITY).
 FT ACT SITE 109 109 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 202 202 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 32 162 BY SIMILARITY.
 FT DISULFID 50 66 BY SIMILARITY.
 FT DISULFID 134 235 BY SIMILARITY.
 FT DISULFID 141 208 BY SIMILARITY.
 FT DISULFID 173 187 BY SIMILARITY.
 FT DISULFID 198 222 BY SIMILARITY.
 FT SITE 196 196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
 SQ SEQUENCE 248 AA; 26087 MW; 78B79DD6FEL5FOCE CRC64;
 Query Match 41.2%; Score 566; DB 1; Length 248;
 Best Local Similarity 45.8%; Pred. No. 2e-39;
 Matches 116; Conservative 39; Mismatches 86; Indels 12; Gaps 7;
 Qy 3 LSIFLLLCVLG-----LSQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRW 56
 Db 1 MKFLVLVAFVAVAFPISEDDDDKIVGGYSCARSAAPYQVSLNSGYHF-CGGSLSISSQW 59
 Qy 57 VLTAHCGSGRYWVRLGHEHSLQDWTQIRHSGFVTHPGYLGASTSHEHDLRLRL 116
 Db 60 VLSAAHCYKSSIQVKGLEYNLAAQDGEQTSSSKVIRHSGY-NANTLN-NDIMLIKLSK 117
 Qy 117 PVRTSSVQPLPLPNDCATAGTECHVSGWGTINHPRPDPDLLOCLNLSIVSHATCHGVY 176
 Db 118 AATLNSYVNTVPLPTSCVTAGTTCILISGWNLTSSGSLYPPDLVCLNAPVLSSSQCSAY 177
 Qy 177 PGRITSNMVCAGGV-PGQDACQSGSGPLVCGVQLGLVSGVSGPCQDGPVYTYIC 235
 Db 178 PGRITSNMVICYLGNGKDCSQSGSGPVVCGVQLGLVSGVSG-IG-CAQKGYPGVYTKVC 235
 Qy 236 KYVDWIRMIMRN 248
 Db 236 NYVSWIKTWSSN 248

RESULT 12

TRYL CHICK
 ID TRY1 CHICK STANDARD; PRT; 248 AA.
 AC Q90627;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Trypsin I-P1 precursor (EC 3.4.21.4).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=95251611; PubMed=7733885;
 RA Wang K., Gan L., Lee I., Hood L.E.;
 RT "Isolation and characterization of the chicken trypsinogen gene family.";
 RL Biochem. J. 307:471-479 (1995).
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: High levels are seen in the pancreas while lower levels are found in the liver, spleen and thymus.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; U15155; AAA79912.1; -.
 DR PIR; S55067; S55067.
 DR HSP; P00763; IDPO.
 DR MEROPS; S01.151; -.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_DOM; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Hydrolase; Serine protease; Digestion; Pancreas; Zymogen;
 KW Calcium-binding; Signal; Multigene family.
 FT SIGNAL 1 15 BY SIMILARITY.
 FT PROPEP 16 25 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 26 248 TRYPSIN I-P1.
 FT ACT SITE 65 65 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT METAL 77 77 CALCIUM (BY SIMILARITY).
 FT METAL 79 79 CALCIUM (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 87 87 CALCIUM (BY SIMILARITY).
 FT ACT SITE 109 109 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 202 202 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 32 162 BY SIMILARITY.
 FT DISULFID 50 66 BY SIMILARITY.
 FT DISULFID 134 235 BY SIMILARITY.
 FT DISULFID 141 208 BY SIMILARITY.
 FT DISULFID 173 187 BY SIMILARITY.
 FT DISULFID 198 222 BY SIMILARITY.
 FT SITE 196 196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
 SQ SEQUENCE 248 AA; 26069 MW; C4CF589912B23D98 CRC64;
 Query Match 41.1%; Score 565; DB 1; Length 248;
 Best Local Similarity 45.5%; Pred. No. 2.4e-39;
 Matches 115; Conservative 41; Mismatches 85; Indels 12; Gaps 7;
 Qy 3 LSIFLLLCVLG-----LSQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRW 56
 Db 1 MKFLVLVAFVAVAFPISEDDDDKIVGGYSCARSAAPYQVSLNSGYHF-CGGSLSISSQW 59
 Qy 57 VLTAHCGSGRYWVRLGHEHSLQDWTQIRHSGFVTHPGYLGASTSHEHDLRLRL 116
 Db 60 VLSAAHCYKSSIQVKGLEYNLAAQDGEQTSSSKVIRHSGY-NANTLN-NDIMLIKLSK 117
 Qy 117 PVRTSSVQPLPLPNDCATAGTECHVSGWGTINHPRPDPDLLOCLNLSIVSHATCHGVY 176
 Db 118 AATLNSYVNTVPLPTSCVTAGTTCILISGWNLTSSGSLYPPDLVCLNAPVLSSSQCSAY 177
 Qy 177 PGRITSNMVCAGGV-PGQDACQSGSGPLVCGVQLGLVSGVSGPCQDGPVYTYIC 235
 Db 178 PGRITSNMVICYLGNGKDCSQSGSGPVVCGVQLGLVSGVSG-IG-CAQKGYPGVYTKVC 235
 Qy 236 KYVDWIRMIMRN 248
 Db 236 NYVSWIKTWSSN 248
 RESULT 13
 ID KLK5 HUMAN STANDARD; PRT; 293 AA.
 AC Q9Y337; Q9H8G8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)
DE (kallikrein-like protein 2) (KLK-L2).
GN KLK5 OR SCTE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stratum corneum;
RX MEDLINE=99445563; PubMed=10514489;
RA Brattsand M., Egelund T.;
RT "Purification, molecular cloning, and expression of a human stratum
RT corneum trypsin-like serine protease with possible function in
RT desquamation.";
RL J. Biol. Chem. 274:30033-30040(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13.3-q13.4.";
RL Anticancer Res. 19:2843-2852(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Faepfer B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be involved in desquamation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in skin, breast, brain and testis.
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC
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CC
CC EMBL; AF168768; AAF03101.1; -
CC EMBL; AF135028; AAD26429.1; -
CC EMBL; AF243527; AAG33358.1; -
CC EMBL; BC008036; AAH08036.1; -
CC HSSP; P00763; 1DPO.

DR MEROPS; S01.017; -
DR Genew; HGNC:6366; KIKS.
DR MIN; 605643; -
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR GO; GO:0008544; P:epidermal differentiation; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys_Ser_crypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00200; TRYD_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 293 KALLIKREIN 5.
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 153 153 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 245 245 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 73 206 BY SIMILARITY.
FT DISULFID 93 109 BY SIMILARITY.
FT DISULFID 178 279 BY SIMILARITY.
FT DISULFID 185 251 BY SIMILARITY.
FT DISULFID 217 231 BY SIMILARITY.
FT DISULFID 241 266 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 25 56 MISSING (IN REF. 3).
SQ SEQUENCE 293 AA; 32020 MW; D92C92F56095946 CRC64;

Query Match 41.1%; Score 564.5; DB 1; Length 293;
Best Local Similarity 45.3%; Pred. No. 3.2e-39;
Matches 107; Conservative 41; Mismatches 83; Indels 5; Gaps 4;

QY 15 SQATPKPIFGTEGRNSQPMQVG-LFEGTSIRCGVLIDHRVLTAAHCSSRYWVRLG 73
DB 60 SDDSSRIINSGDCDMHTQPAALLLRPNQLYCGAVLHPQWLLTAACHKRVFVRLG 119
QY 74 EHSLSOLDWTQIRHSGF-SVTHPGYLCASTSHEHDLRLRLPVRVTSSVQPLPLPND 132
DB 120 HYSLSPVYESQOMFQGVKSIPHGK--SHFGHNDLMLIKLNRIRPTKDVRLNVSSH 177
QY 133 CATAGTECHVSGWGITNHRNPPFDLLQCLNLSIVSHATCHGVTPGRITSNMVCAGGVPG 192
DB 178 CPSAGTKCLVSGWGTGTPVHFPRKVLQCLNLSVLSQKRCEDAYPRQIDDTMFCAGDKAG 237
QY 193 ODACQGDGSGPLVCGGVLOGVLSVSGVSGCGDGPVGYTVYICKYVDVIMRMNN 248
DB 238 RDSQCGSGGPPVNCNGSLQGLVSMGDY-PCARPNRPGVITNLCKFTKVIQETIQAN 292

RESULT 14
KLKA HUMAN
ID KLKA HUMAN STANDARD; PRT; 276 AA.
AC Q43440; Q99920; Q9GZW9;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Kallikrein 10 precursor (EC 3.4.21.-) (Protease serine-like 1) (Normal
DE epithelial cell-specific 1).
GN KLK10 OR PRS10 OR NES1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epithelium;

01-NOV-1997 (Rel. 35, last sequence update)
10-OCT-2003 (Rel. 42, last annotation update)
Trypsin precursor (SC 3.4.21.4).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
RA Wang K., Lytle L., Gan L., Hood L.E.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: Belongs to peptidase family S1.

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DR EMBL; U72330; AAB17274.1; -.
DR HSPF; P00763; IDPO.
DR MEROPS; S01.258; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Digestion; Zymogen; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 15 BY SIMILARITY.
FT PROPEP 16 21 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 22 244 TRYPSIN.
FT ACT_SITE 61 61 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT METAL 73 73 CALCIUM (BY SIMILARITY).
FT METAL 75 75 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 83 83 (BY SIMILARITY).
FT METAL 83 83 CALCIUM (BY SIMILARITY).
FT ACT_SITE 105 105 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 198 198 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 28 158 BY SIMILARITY.
FT DISULFID 46 62 BY SIMILARITY.
FT DISULFID 130 231 BY SIMILARITY.
FT DISULFID 137 204 BY SIMILARITY.
FT DISULFID 169 183 BY SIMILARITY.
FT DISULFID 194 218 BY SIMILARITY.
FT SITE 192 192 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 244 AA; 26079 MW; C63F29CB3300B323 CRC64;
Query Match 41.0%; Score 563; DB 1; Length 244;
Best Local Similarity 45.0%; Pred. No. 3.5e-39;
Matches 112; Conservative 46; Mismatches 83; Indels 8; Gaps 5;
QY 3 LSFILLCVLGLSQA--ATPKLFNGTECGRNPQWGLFEGTSLRCGGVLIDHRWLTA 60
DB 1 MKFLVILVLLGAVAFEDDDKLVGGFTCAKNVAPVQVSLNAGYHP--CGSLINSQWVSA 59
QY 61 AHCSSGRYVWRLGHSLSQLDWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLPLRVV 120
DB 60 AHCYKSRIQVRLGHEHNLNEGTEQFIDSKVIKHPNY--NGRNLDNDIMLIKLTARL 117
QY 121 TSSVQLEPLPNDCATAGTCHVSGWGITNHRPNPPDILQCLNLSIVSHATCHGVYPGRI 180
DB 118 SANIQSVPLPSACASAGTNCLISGMGNTLSSGTNYPDLLQCLNAPILTDSQCSNYPGEI 177

Qy 181 TSNMVCAGGYP--GQDACQGSBSGGLVCGGVLOGLVSWGSVGPCQDGIPIGVYTIKYYD 239
Db 178 TKMFCAGFLAGKQSCQSDSGGPFVWCNGQLQGVVSWGY--GCAQRNYPGVYITKVCNFVT 235
Qy 240 WIRMIMRNN 248
Db 236 WIQSTISSN 244

Search completed: June 15, 2004, 16:15:37
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: June 15, 2004, 16:13:26 ; Search time 20 Seconds
(without alignments)
1192.775 Million cell updates/sec

Title: US-10-006-856A-194
Perfect score: 1374
Sequence: 1 MGLSIFLLCLVGLGSAATP.....GVYTIKVDWIRMIRNN 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

1: Pir1: *
2: Pir2: *
3: Pir3: *
4: Pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622.5	45.3	260	2 I56559	neuropsin - mouse
2	569.5	41.4	248	2 S55066	trypsin (EC 3.4.21)
3	567	41.3	248	2 S55067	trypsin (EC 3.4.21)
4	561	40.8	231	1 TRPQTR	trypsin (EC 3.4.21)
5	555	40.4	243	2 A35871	trypsin (EC 3.4.21)
6	555	40.4	253	2 A53968	serine proteinase
7	553	40.2	246	2 B25528	trypsin (EC 3.4.21)
8	552	40.2	229	1 TRBOTR	trypsin (EC 3.4.21)
9	550	40.0	247	2 S13813	trypsin (EC 3.4.21)
10	546	39.7	247	1 TRDGC	trypsin (EC 3.4.21)
11	545	39.7	246	1 TRDGC	trypsin (EC 3.4.21)
12	544.5	39.6	247	2 A27547	trypsin (EC 3.4.21)
13	543	39.5	246	1 TRRT1	trypsin (EC 3.4.21)
14	540	39.3	238	2 S31779	trypsin (EC 3.4.21)
15	533.5	38.8	247	2 S05494	trypsin (EC 3.4.21)
16	532	38.7	246	1 TRRT2	trypsin (EC 3.4.21)
17	527.5	38.4	261	2 A31136	tissue kallikrein
18	524	38.1	232	1 KQPG	tissue kallikrein
19	520.5	37.9	261	2 A25606	tissue kallikrein
20	519	37.8	246	2 JQ1471	trypsin (EC 3.4.21)
21	518	37.7	246	2 JQ1472	trypsin (EC 3.4.21)
22	518	37.7	261	2 A34079	tissue kallikrein
23	513.5	37.4	231	2 S31778	trypsin (EC 3.4.21)
24	513.5	37.4	239	2 A27207	tissue kallikrein
25	511.5	37.2	261	2 S45303	tissue kallikrein
26	510.5	37.2	261	1 NQMSG	7S nerve growth fa
27	508	37.0	242	2 S31775	trypsin (EC 3.4.21)
28	508	37.0	242	2 S31776	trypsin (EC 3.4.21)
29	503	36.6	260	2 A37938	tissue kallikrein

30	503	36.6	263	2 S15686	tissue kallikrein
31	502	36.5	259	2 B31136	tissue kallikrein
32	501	36.5	247	1 B25852	trypsin (EC 3.4.21)
33	499.5	36.4	241	2 S39048	trypsin (EC 3.4.21)
34	496.5	36.1	261	1 TRMSM5	tissue kallikrein
35	496	36.1	242	2 S49489	trypsin (EC 3.4.21)
36	495.5	36.1	257	2 S33772	tissue kallikrein
37	495.5	36.1	261	2 S01971	tissue kallikrein
38	494.5	36.0	247	1 A25852	trypsin (EC 3.4.21)
39	493	35.9	262	1 KQHU	tissue kallikrein
40	491.5	35.8	240	2 S39047	trypsin (EC 3.4.21)
41	491	35.7	256	1 NGMSA	7S nerve growth fa
42	490.5	35.7	229	1 TRDFS	trypsin (EC 3.4.21)
43	490.5	35.7	261	2 A41020	tissue kallikrein
44	489	35.6	244	2 A44284	tissue kallikrein
45	485.5	35.3	261	2 JF0236	tissue kallikrein

ALIGNMENTS

RESULT 1

I56559
neuropsin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: I56559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nish J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease
A:Reference number: I56559; MUID:95348817; PMID:7623137
A:Accession: I56559
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: GB:D30785; NID:91648847; PIDN:BAA06451.1; PID:g1020091
C:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRY>

Query Match 45.3%; Score 622.5; DB 2; Length 260;

Best Local Similarity 49.0%; Pred. No. 1.4e-43;

Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

QY	5	IFLLLCV---	LGISQATPKIFNGTEGNSOPQVGLPEGTSLRCGGVLIDRWLTAA	61
DB	13	ILLLEFGAWAGUTRAQGSKILEGRCIHSQWQAALQGERLICGGVLVGRWLTAA	72	
QY	62	HCSGRIYVRLGHEHSLQDLWTQIRHSGFSVTHPGYLGAS-TSHEHDLRLRLPVRV	120	
DB	73	HCKKQKYSVRLGDHSLQSRDQPEQIQVAQSIQHPCCYNNSPRDSHDMILRLQNSANL	132	
QY	121	TSSVQPLPLPNDCATAGTECHVSGWGIYTHPRNPFDDLLQCLNLSIVSHATCHGVVPGRI	190	
DB	133	GDKVPVQLANLCPKVGQKCIISGWTVTSPQENFNTLNCAEVKTIYQNKCEATPGKI	192	
QY	181	TSNMVACGGVPGQDACQGSGLVCGVLQGLVSGVSGPCGQDGIPIGVYTIKCYVDW	240	
DB	193	TEGMVACGNSGADTCQGSGLVCDGLQGITSWGSDPCGKPKPGVYTIKCYTTW	251	
QY	241	IRMIMRN	247	
DB	252	IKKTMND	258	

RESULT 2

S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N:Alternate names: trypsinogen II
C:Species: Gallus gallus (chicken)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
C:Accession: S55066; S72347
R:Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995

F:60,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 40.8%; Score 561; DB 1; Length 231;
Best Local Similarity 46.7%; Pred. No. 1.3e-38;
Matches 107; Conservative 39; Mismatches 77; Indels 6; Gaps 4;

QY 21 KIFNGTECGRNSQPMQVGLPEGTSLRCGVLIDHRWVLTAAHCSGSRVWRLGHEHLSOL 80
DB 8 KIVGGYTCAANSIPYQVSLNSGSHF-CGGLINSQVWVSAACHYKSRIOVRLGHEHIDL 66
QY 81 DTEQIRHSGFSTHPCYLCASTSHEHDLRLRLPVRVTSVQPLPNDCAATGTC 140
DB 67 EGNEQFINAAKIITHFNFG--NTLNDIMLKLSPPATLNSRVATVSPRSCAAAGTTC 124
QY 141 HVSGWGITNHRNPPFDLLLOCLMSLVSHATCHGVTPGRITSNMVCAGVP-GQDACQGD 199
DB 125 LISGWNKTSKSSSYPSLLQCLKAPVLSDSKSSYPGQITGNMIVCGFLEGKDCQSD 184
QY 200 SGSPVLCGVGLQGLVSWGSGVPCQDGIQGVYTYICKYVDWMIRMNN 248
DB 185 SGGPVVVCNGLOQIVSWGY-GCAQKNKPGVYTKVCNVNWIQQTIAAN 231

RESULT 5
A35871

trypsin (EC 3.4.21.4) precursor, pancreatic - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 04-Mar-2000
C:Accession: A35871; S12117
R:Shi, Y.B.; Brown, D.D.
Genes Dev. 4, 1107-1113, 1990
A:Title: Developmental and thyroid hormone-dependent regulation of pancreatic genes in X
A:Reference number: A35871; MUID:91007255; PMID:2210372
A:Accession: A35871
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-243 <SHI>
A:Cross-references: EMBL:X53458; NID:g65162; PIDN:CAA37538.1; PID:g65163
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; protein digestion; serine proteinase
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-20/Domain: activation peptide #status predicted <APT>
F:21-236/Domain: trypsin homology <TRY>
F:26-243/Product: trypsin I #status predicted <MAT>
F:27-157,45-61,129-230,136-203,168-182/Disulfide bonds: #status predicted
F:60,104,197/Active site: His, Asp, Ser #status predicted

Query Match 40.4%; Score 555; DB 2; Length 243;
Best Local Similarity 45.7%; Pred. No. 4.3e-38;
Matches 113; Conservative 42; Mismatches 82; Indels 10; Gaps 6;

QY 6 FLLLCVLGSLQAAT---PKIFNGTECGRNSQPMQVGLPEGTSLRCGVLIDHRWVLTAAH 62
DB 3 FLLLCVL-LGAAAFDDDKIIGATCAKSSVPYIVSLNSGYH-CGGLITNQWVYSAH 60
QY 63 CGSRVWVRLGHEHLSQLDWTEQIRHSGFSTHPCYLCASTSHEHDLRLRLPVRVTS 122
DB 61 CYKASTQVRLGHEHLSQLDWTEQIRHSGFSTHPCYLCASTSHEHDLRLRLPVRVTS 118
QY 123 SVQPLPNDCAATGATGCHVSGWGITNHRNPPFDLLLOCLNLSIVSHATCHGVTPGRITS 182
DB 119 AVNTVPLPSCSAAGTSLGSGWNTLNSGNSYFDLLQCLNAPILNTAOCNSAYPGEITA 178
QY 183 NMVCAGVP-GQDACQGDSCGGLVCGVGLQGLVSWGSGVPCQDGIQGVYTYICKYVDWI 241
DB 179 NMTCVGMEGKDCQGDSCGGLVCGVGLQGLVSWGSGVPCQDGIQGVYTYICKYVDWI 236
QY 242 RMTMRNN 248
DB 237 QNTIAAN 243

RESULT 6

A53968
serine proteinase SCCE precursor - human
N:Alternate names: stratum corneum chymotryptic enzyme
C:Species: Homo sapiens (man)
C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C:Accession: A53968
R:Hansson, L.; Stromqvist, M.; Baekman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, J. Biol. Chem. 269, 19420-19426, 1994
A:Title: Cloning, expression, and characterization of stratum corneum chymotryptic en:
A:Reference number: A53968; MUID:94308225; PMID:8034709
A:Accession: A53968
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-253 <HAN>
A:Cross-references: GB:L33404; NID:g521214; PIDN:AA37551.1; PID:g532504
C:Genetics:
A:Gene: GDB:PRSS6; SCCE
A:Cross-references: GDB:377730
A:Map position: 7q35-7q35
A:Superfamily: trypsin; trypsin homology
F:30-245/Domain: trypsin homology <TRY>

Query Match 40.4%; Score 555; DB 2; Length 253;
Best Local Similarity 44.6%; Pred. No. 4.5e-38;
Matches 115; Conservative 37; Mismatches 90; Indels 16; Gaps 6;

QY 1 MGLSIFLLLCVGLS-----QAATPKIFNGTECGRNSQPMQVGLPEGTSLRCGVL 52
DB 1 MARSLLPLQLLLSLALETAGEEAQGDKIIDGAPCARSHPWQVALLSGNQLHCGGLV 60
QY 53 DHRWVLTAAHCSGSRVWVRLGHEHLSQLDWTEQIRHSGFSTHPCYLCASTSHEHDLRL 112
DB 61 NERWVLTAAHCSGSRVWVRLGHEHLSQLDWTEQIRHSGFSTHPCYLCASTSHEHDLRL 116
QY 113 RLRLPVRVTSVQPLPNDCAATGCHVSGWGITNHRNPPFDLLLOCLNLSIVSHATC 172
DB 117 KLNSQARLSMVKVRLPSCRPPGTTCTVSGWGITTSDDVTFPSDLMLCVDVKLISPDQC 176
QY 173 HGVPGRITSNMVCAGVP--QDACQGDSCGGLVCGVGLQGLVSWGSGVPCQDGIQGV 230
DB 177 TKVYKDLLENSMLCA-GIPDSKKNACNGDSGGPLVCRGTQGLVSWGTF-PCGQNDPGV 234
QY 231 YTVICKYVDWMIRMNN 248
DB 235 YTVQCKFTKINDTKKH 252

RESULT 7
B25528

trypsin (EC 3.4.21.4) precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999
C:Accession: B25528
R:Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A:Title: Sequence organisation and transcripational regulation of the mouse elastase I
A:Reference number: A93646; MUID:87066713; PMID:3641189
A:Accession: B25528
A:Molecule type: mRNA
A:Residues: 1-246 <STE>
A:Cross-references: GB:X04574; NID:g54918; PIDN:CAA28243.1; PID:g54919
C:Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-246/Product: trypsin #status predicted <MAT>
F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 40.2%; Score 553; DB 2; Length 246;
Best Local Similarity 44.7%; Pred. No. 6.3e-38;
Matches 113; Conservative 45; Mismatches 81; Indels 14; Gaps 7;


```

119 RVTSVQPLPNDNCATAGTECHVSQWGINTHPRNPFDDLLQCLNLUSIVSHATCHGVYFG 178
      : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | :
118 TLNSRVSAIALPKSCPAAGTQCILISGWGNTQSIGNQYPDVLOCLKAPILSDSVCRNAYPG 177
      : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | :
179 RITSNNVCACGVP-GGDACGGDSGGPLVCGGLVQLGSWSGSPCCGQDGI PGVTYVICKY 237
      : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | :
178 QISSNMCLGYMGKKDKSCGDSGGPVVNGELQGVSWSGA--CCAQKKGPGVSPKVCKY 235
      : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | :
238 VDWIRIMTRNN 248
      ||| : |
236 VSWIQQTIAAN 246
      ||| : |

RESULT 12
A27547
C:Species: Rattus norvegicus (Norway rat)
C:CDate: 30-Jun-1998 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999
C:Accession: A27547
R:Fletcher, T.S.; Alhadef, M.; Craik, C.S.; Largman, C.
Biochemistry 26, 3081-3086, 1987
A:Title: Isolation and characterization of a cDNA encoding rat cationic trypsinogen.
A:Reference number: A27547; PMID:8721609; PMID:3607011
A:Accession: A27547
A:Molecule type: mRNA
A:Residues: 1-247 <FLE>
A:A-Cross-references: GB:M16624; NID:g206498; PIDN:AAA41985.1; PID:g206499
C:Superfamily: trypsin; protein digestion; serine proteinase
C:Keywords: calcium binding; hydrolyase; protein digestion; trypsin homologY
F:25-240/Domain: trypsin homology <TRY>
F:31-161,49-65,133-234,140-207,172-186/disulfide bonds: #status predicted
F:64,108,201/Active site: His, Asp, Ser #status predicted
F:76,78,81,86/Binding site: Calcium (Glu, Asn, Val, Glu) #status predicted
```

```

Desc Local Similarity 45.3%; Fied. NO. 3.1e-37; Matches 109; Conservative 43; Mismatches 89; Indels 11; Gaps 5;

QY      3  LSIPELLCVLGLSQA-----TPKIFNGTCGRNSOPWQVLPEGTSLRGGVLIIDHRWV 57
Ddb      1  MKALIFLAFIAGAAVALPLDDDDKIVGGYTCQKNSLPYQVSLNAGYHF-CGGLINSQWV 59

QY      58  LTAACHCGSRYYWVLGSHSLSQLDWTQIIRHSGFSVTHPGYLGAOSTSHBDLRLRLP 117
Ddb      60  VSAACHYKSRIQVRLGEHNDVVEGGEQFIDAAKIIRHPSY--NANTFDNDIMLIKNSP 117

QY      118  VRVTSVQPLPLPNDCATAGTECHVSWGITNPRPFPDLOLCLNLISIVSHATCHGVYP 177
Ddb      118  ATLSRSYTVSLPRSCGSSGSKCLVSWGNTLSGTYNPSLLQCLDAPVLSDSCKSSYP 177

QY      178  GRITSNMVCAGVF-GDACAQDGSGLVCGGVQLGLVSMGVSVPCCQDQIGPVYTVCK 236
Ddb      178  GRITSNMFCFLGEGKDSQGDSGGPVVCNGQLQGVVSMGY--GCAQKGKPGVYTKVCN 235

QY      237  YVDWIRMIMRNN 248
Ddb      236  YVNMIQQTVAAN 247

RESULT 13
TRRT1
N:Altearnate names: trypsinogen I
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 24-Sep-1999
C:Accession: B22657; A00948
R:Cralk, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J: Biol. Chem. 259, 14255-14264, 1984
A:Title: Structure of two related rat pancreatic trypsin genes.
A:Reference number: A22657; MUID:85054880; PMID:6094547
A:Accession: B22657
A:Molecule type: DNA
A:Residues: 1-246 <CR>

```

A;Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
 A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17
 B;Macdonald, R.J.; Stary, S.J.; Swift, G.H.
 J. Biol. Chem. 257, 9724-9732, 1982
 A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of
 A;Reference number: A00948; MUID:82265624; PMID:6896710
 A;Accession: A00948
 A;Molecule type: mRNA
 A;Residues: 1-246 <MAC>
 A;Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
 C;Genetics:
 A;Introns: 14/1; 67/2; 152/1; 197/3
 C;Superfamily: trypsin; trypsin homology
 C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
 F;1-15/Domain: signal sequence #status predicted <SIG>
 F;16-23/Domain: activation peptide #status predicted <APT>
 F;24-246/Product: trypsin I #status predicted <ENZ>
 F;24-239/Domain: trypsin homology <TRY>
 F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
 F;63,107,200/Active site: His, Asp, Ser #status predicted
 F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.5%; Score 543; DB 1; Length 246;
 Best Local Similarity 44.5%; Pred. No. 4.1e-37;
 Matches 110; Conservative 47; Mismatches 76; Indels 14; Gaps 7;

Qy 3 LSIPELLCVLGLSQA---ATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWVL 58
 Db 1 MSALLILALVGAFAFLEDDDKIVGGVTCPEHSVPYQVSLNSGVHP-CGSLINDQVWV 59
 Qy 59 TAAHCSGRYVWRGLGHSLSOLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPLV 118
 Db 60 SAAHCYKSRIOVRLGHNINVLGEQEFINAAKIKHENY--SSWTLNDIMLIKSSPV 117
 Qy 119 RVTSSVQPLPNDNCATAGTCHVSGWG--ITNPRNPFLLQCLNLSIVSHATCHGVY 176
 Db 118 KINARVAPVALPSACAPAGTQCLISGWTLSGNNV--PDLLQCVAPVLISQADCEAY 175
 Qy 177 PGRITSNMVCAGVP-GQDACQGGSGPLVCGGLVSGVSPGCCQDGPVYTVIC 235
 Db 176 PGEITSSMICVGLFEGGKDCQSDSGGPPVNCGLQIVSGWY--GCALPNPFGVYTKV 233
 Qy 236 KYVDWIR 242
 Db 234 NFVGMQ 240

RESULT 14

trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)
 C;Species: Salmo salar (Atlantic salmon)
 C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
 C;Accession: S66657; S31779
 R;Male, R.; Lorens, J.B.; Smalas, A.O.; Torrisen, K.R.
 Eur. J. Biochem. 232, 677-685, 1995
 A;Title: Molecular cloning and characterization of anionic and cationic variants of tryp
 A;Reference number: S66657; MUID:96035908; PMID:7556223
 A;Accession: S66657
 A;Molecule type: mRNA
 A;Residues: 1-238 <MAL>

A;Cross-references: EMBL:X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388
 C;Superfamily: trypsin; trypsin homology
 C;Keywords: hydrolase; serine proteinase
 F;1-7/Domain: signal sequence (fragment) #status predicted <SIG>
 F;8-15/Domain: activation peptide #status predicted <APT>
 F;16-238/Product: trypsin III #status predicted <MAT>
 F;16-231/Domain: trypsin homology <TRY>
 F;22-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted
 F;55,99,192/Active site: His, Asp, Ser #status predicted

Query Match 39.3%; Score 540; DB 2; Length 238;
 Best Local Similarity 47.2%; Pred. No. 7e-37;
 Matches 108; Conservative 37; Mismatches 78; Indels 6; Gaps 4;

Qy 21 KIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWLTAAHCSGRYVWRGLGHSLSQL 80
 Db 15 KIVGYECRKNSSAYQASLQSGVHP-CGSLISSTWVWSAAHCYKSRIOVRLGSHNIAVN 73
 Qy 81 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPLRVVTSSVQPLPNDNCATAGTTC 140
 Db 74 EGTEQFIDSVKVIMHPSY--NSRNLNDIMLIKSPASLNSYVSTVALPSSCASSGTRC 131
 Qy 141 HVSQWGTNHPNRPFPDQLCLNLSIVSHATCHGVYPRITSNMVCAGVP-GQDACQGD 199
 Db 132 LVSGWNLGSSSNYPDLTLCLDPLILSSSSCSNAYPGQITSNMFCAGFMEGGKDCQGD 191
 Qy 200 SGGPLVCGGLVGLVSGVSPGCCQDGPVYTVICKYVDWIRIMENN 248
 Db 192 SGGPVCNQLQGVVSWGY--GCAQRNKPQVYTKVCNYSWISWTSSN 238

RESULT 15

S05494

trypsin (EC 3.4.21.4) IV precursor - rat
 A;Alternate names: 23K protein; trypsinogen IV precursor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Jun-1999
 C;Accession: S05494
 R;Luettcke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.
 Nucleic Acids Res. 17, 6736, 1989
 A;Title: A fourth trypsinogen (P23) in the rat pancreas induced by CCK.
 A;Reference number: S05494; MUID:89386010; PMID:2780302
 A;Accession: S05494
 A;Molecule type: mRNA
 A;Residues: 1-247 <LUE>
 A;Cross-references: EMBL:X15679; NID:g56813; PIDN:CAA33718.1; PID:g56814
 C;Superfamily: trypsin; trypsin homology
 C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen
 F;1-15/Domain: signal sequence #status predicted <SIG>
 F;16-23/Domain: activation peptide #status predicted <APT>
 F;24-247/Product: trypsin IV #status predicted <MAT>
 F;24-240/Domain: trypsin homology <TRY>
 F;30-161,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted
 F;64,108,201/Active site: His, Asp, Ser #status predicted
 F;76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 38.8%; Score 533.5; DB 2; Length 247;
 Best Local Similarity 43.4%; Pred. No. 2.5e-36;
 Matches 109; Conservative 41; Mismatches 94; Indels 7; Gaps 4;

Qy 1 MGLSIP--LLLCVLGLSQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWVL 58
 Db 1 MKSIFFAFLGAVALFVNDKDKIVGGVTCPKHLVYQVSLHDGISHQCGSLISDQVWL 60
 Qy 59 TAAHCSGRYVWRGLGHSLSOLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPLV 118
 Db 61 SAAHCYKRLQVRLGHNINVLGEQEFIDAELIRPEY--NKOTLDNDIMLIKSPKA 118
 Qy 119 RVTSSVQPLPNDNCATAGTCHVSGWGTNHPNRPFPDQLCLNLSIVSHATCHGVYYP 178
 Db 119 VLNSQVSTVSLPRSCASTDAQCLVSGWGTVSIQKYPALLQCLLEAPVLSSACKSYPG 178
 Qy 179 RITSNMVCAGVP-GQDACQGGSGPLVCGGLVSGVSPGCCQDGPVYTVICKY 237
 Db 179 QITSNMFLGLEGGKDCQSDSGGPPVNCGETQGIIVSGSV--CAMRGPQVYTKVCNY 236
 Qy 238 VDWIRIMLRNN 248
 Db 237 LSWIQETMANN 247

Search completed: June 15, 2004, 16:17:09
 Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 16:10:36 ; Search time 60 seconds
(without alignments)
1167.863 Million cell updates/sec

Title: US-10-006-856A-194

Perfect score: 1374

Sequence: 1 MGLSIFLLCVLGLSQATP.....GVVTYICKYVDWIRMIWENN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1374	100.0	248	3 AAB21304	Aab21304 Human KIK
2	1374	100.0	248	3 AAB24428	Aab24428 Human PRO
3	1374	100.0	248	3 AAB24032	Aab24032 Human PRO
4	1374	100.0	248	3 AAY93193	Aay93193 Human PRO
5	1374	100.0	248	4 RAM23994	Aam23994 Human EST
6	1374	100.0	248	4 AAB66142	Aab66142 Protein o
7	1374	100.0	248	6 ABO33635	Abo33635 Novel hum
8	1374	100.0	248	7 ABO44488	Abo44488 Human sec
9	1374	100.0	248	7 ABO33512	Abo33512 Novel hum
10	1374	100.0	248	7 ADC18063	Adc18063 Human PRO
11	1374	100.0	248	7 ADD70709	Add70709 Human sec
12	1374	100.0	248	7 ADD3786	Add3786 Human sec
13	1374	100.0	248	7 ADD70232	Add70232 Human sec
14	1374	100.0	248	7 ADD38353	Add38353 Human sec
15	1374	100.0	248	7 ADD39309	Add39309 Human sec
16	1374	100.0	248	7 ADD38832	Add38832 Human sec
17	1374	100.0	248	7 ADD40263	Add40263 Human sec
18	1374	100.0	248	7 ADE50484	Ade50484 Human sec
19	1374	100.0	248	7 ADE20096	Ade20096 Human sec
20	1374	100.0	248	7 ADE50007	Ade50007 Human sec
21	1374	100.0	248	7 ADE21565	Ade21565 Human sec
22	1367	99.5	248	6 AAO29516	Aao29516 Human kal
23	1301	94.7	254	3 AAB21303	Aab21303 Human KIK
24	1301	94.7	254	5 ABG66676	Abg66676 Human nov
25	1019	74.2	184	3 AAB21301	Aab21301 Human KIK

ALIGNMENTS

RESULT 1

AAB21304
ID AAB21304 standard; protein; 248 AA.

XX AAB21304;

DT 02-FEB-2001 (first entry)

XX Human KIK-L5 protein #4.

XX Human; KIK-L1; KIK-L2; KIK-L3; KIK-L4; KIK-L5; KIK-L6;

KW kallikrein-like protein; serine protease; cytostatic; cancer;

KW prostrate cancer.

OS Homo sapiens.

XX WO200053776-A2.

XX PD 14-SEP-2000.

XX 09-MAR-2000; 2000WO-CA000258.

XX 11-MAR-1999; 99US-0124260P.

XX 01-APR-1999; 99US-0127386P.

XX 21-JUL-1999; 99US-0144919P.

XX (MOUN) MOUNT SINAI HOSPITAL.

XX Yousef GM, Diamandis EP;

XX WPI; 2000-587440/55.

XX N-PSDB; AAA95944.

XX New kallikrein-like (KIK-L) proteins for diagnosing and treating KIK-L protein mediated disorders, especially cancer.

XX Claim 12; Page 172; 184pp; English.

XX The present sequence is one of four alternatively spliced kallikrein-like proteins encoded by the human KIK-L4 gene. Kallikreins and kallikrein-like proteins are a subgroup of the serine protease enzyme family. They catalyze the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding kallikrein-like proteins KIK-L1, KIK-L2, KIK-L3, KIK-L4, KIK-L5 and KIK-L6 have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of cancers, especially prostate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used

CC to treat conditions mediated by the kallikrein-like proteins

XX Sequence 248 AA;

Query Match 100.0%; Score 1374; DB 3; Length 248;
 Best Local Similarity 100.0%; Pred. No. 3.8e-98;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVGLGSLQATPKIFNGTECGRNQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
 Db 1 MGLSIFLLLCVGLGSLQATPKIFNGTECGRNQPMQVGLFEGTSLRCGGVLIDHRWLTA 60

QY 61 AHCSGSRYWVRLGHSLSOLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
 Db 61 AHCSGSRYWVRLGHSLSOLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120

QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
 Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180

QY 181 TSNMVCAGVPGQDACQDGGSLVCGVGLQGLVSWGSGVPGCGQDGIPIGVYTYICKYVDW 240
 Db 181 TSNMVCAGVPGQDACQDGGSLVCGVGLQGLVSWGSGVPGCGQDGIPIGVYTYICKYVDW 240

QY 241 IRMIMRNN 248
 Db 241 IRMIMRNN 248

RESULT 2

AAB24428
 ID AAB24428 standard; protein; 248 AA.

XX AC AAB24428;

XX DT 07-NOV-2000 (first entry)

XX DE Human PRO1303 protein sequence SEQ ID NO:203.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
 KW cytoskeletal; gene therapy; vaccine.

XX Homo sapiens.

OS WO200032221-A2.

FN 08-JUN-2000.

XX PF 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1998; 98WO-US025108.

XX 16-DEC-1998; 98US-0112850P.

XX 12-JAN-1999; 99US-0115554P.

XX 08-MAR-1999; 99WO-US005028.

XX 12-MAR-1999; 99US-0123957P.

XX 28-APR-1999; 99US-0131445P.

XX 14-MAY-1999; 99US-0134287P.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 05-OCT-1999; 99WO-US021547.

XX 29-OCT-1999; 99WO-US023089.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
 PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
 PI Smith V, Watanabe CK, Williams PM, Wood WI;

XX WPI; 2000-412154/35.

DR N-PSDB; AAA77671.

XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
 and treating diagnosing a cardiovascular, endothelial or angiogenic
 disorders in mammals.

PS Claim 72; Fig 82; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides
 useful for preventing, diagnosing and treating diagnosing a
 cardiovascular, endothelial or angiogenic disorder in mammals by
 modulating cell proliferation, angiogenesis and cardiovascularisation,
 and for identifying agonists and antagonists of these processes. The
 nucleic acids and the proteins they encode may be used in the prevention,
 treatment and diagnosis of diseases associated with inappropriate PRO
 expression such as cardiovascular, endothelial or angiogenic disorders in
 mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
 example, the nucleic acids (NCs) and vectors containing them and the PRO
 polypeptide may be used to treat disorders associated with decreased PRO
 expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
 nucleotide and protein sequences used in the exemplification of the
 present invention

XX Sequence 248 AA;

Query Match 100.0%; Score 1374; DB 3; Length 248;
 Best Local Similarity 100.0%; Pred. No. 3.8e-98;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVGLGSLQATPKIFNGTECGRNQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
 Db 1 MGLSIFLLLCVGLGSLQATPKIFNGTECGRNQPMQVGLFEGTSLRCGGVLIDHRWLTA 60

QY 61 AHCSGSRYWVRLGHSLSOLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
 Db 61 AHCSGSRYWVRLGHSLSOLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120

QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
 Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180

QY 181 TSNMVCAGVPGQDACQDGGSLVCGVGLQGLVSWGSGVPGCGQDGIPIGVYTYICKYVDW 240
 Db 181 TSNMVCAGVPGQDACQDGGSLVCGVGLQGLVSWGSGVPGCGQDGIPIGVYTYICKYVDW 240

QY 241 IRMIMRNN 248
 Db 241 IRMIMRNN 248

RESULT 3

AAB24032

ID AAB24032 standard; protein; 248 AA.

XX AC AAB24032;

XX 25-JAN-2001 (first entry)

XX Human PRO1303 protein sequence SEQ ID NO:33.

XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 XX identification; tumourigenesis; anticancer; detection.

XX Homo sapiens.

OS WO200053750-A1.

XX 14-SEP-2000.

XX PF 02-DEC-1999; 99WO-US028551.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 29-OCT-1999; 99US-0162506P.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1999; 99WO-US028634.
XX PA (GETH) GENENTECH INC.
XX PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
XX DR WPI; 2000-594320/56.
XX DR N-FSDB; AAC58114.
XX PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit
XX PT the growth of tumors in mammals, and to identify inhibitors of PRO
XX PT polypeptide activity or expression.
XX PS Claim 61; Fig 24; 226pp; English.
XX CC The present invention describes an antibody that binds to a human protein
CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
CC PRO1927; PRO3567; PRO1293; PRO1303; PRO4354; PRO4397;
CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
CC activity and can be used to diagnose tumours in mammals, by detecting
CC complex formation when the antibody is contacted with test cells.
CC Increased expression of genes encoding (I) can also be detected to
CC diagnose tumours. Agents which inhibit the activity of (I), especially
CC the antibodies, or an antisense oligonucleotide which hybridises to genes
CC encoding (I), can be used to inhibit tumour growth, preferably by
CC inducing cell death. Methods from the present invention can be used to
CC identify compounds which inhibit the biological activity of (I). AAC58019
CC to AAC58102 represent PCR primers and hybridisation probes used in
CC examples from the present invention for human PRO sequences. AAC58103 to
CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
CC protein sequences given in the exemplification of the present invention
XX Sequence 248 AA;
XX SQ
Query Match 100.0%; Score 1374; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSIFLLLCVILGSLQAATPKIFNGTECGNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
DB 1 MGLSIFLLLCVILGSLQAATPKIFNGTECGNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
QY 61 AHCSGRYVVRGHEHSLDQTEQIRHGSFVTHPGYLCASTSHEHDLRLRLPVRV 120
DB 61 AHCSGRYVVRGHEHSLDQTEQIRHGSFVTHPGYLCASTSHEHDLRLRLPVRV 120
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPFDLLQCLNLSIVSHATCHGVYPGRI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPFDLLQCLNLSIVSHATCHGVYPGRI 180
QY 181 TSNMVCAGVPGDQACQSGGGLVCGVLOGLVSGVSPCCGQDGI PGVYTVICKYVDW 240
DB 181 TSNMVCAGVPGDQACQSGGGLVCGVLOGLVSGVSPCCGQDGI PGVYTVICKYVDW 240
QY 241 IRIMENN 248
DB 241 IRIMENN 248
RESULT 4
AAAY99393
ID AAAY99393 standard; protein; 248 AA.
XX
AC AAAY99393;
XX DT 08-AUG-2000 (first entry)
XX PR 30-SEP-1998; 98US-0102487P.
XX PR 30-SEP-1998; 98US-0102570P.
XX DE Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.
XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
XX OS transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX OS Homo sapiens.
XX PN WO200012708-A2.
XX PD 09-MAR-2000.
XX PF 01-SEP-1999; 99WO-US020111.
XX PR 01-SEP-1998; 98US-0098716P.
XX PR 01-SEP-1998; 98US-0098749P.
XX PR 01-SEP-1998; 98US-0098750P.
XX PR 02-SEP-1998; 98US-0098803P.
XX PR 02-SEP-1998; 98US-0098821P.
XX PR 02-SEP-1998; 98US-0098843P.
XX PR 02-SEP-1998; 98US-0098536P.
XX PR 02-SEP-1998; 98US-0099596P.
XX PR 02-SEP-1998; 98US-0099598P.
XX PR 02-SEP-1998; 98US-0099602P.
XX PR 02-SEP-1998; 98US-0099642P.
XX PR 02-SEP-1998; 98US-0099741P.
XX PR 10-SEP-1998; 98US-0099754P.
XX PR 10-SEP-1998; 98US-0099763P.
XX PR 10-SEP-1998; 98US-0099792P.
XX PR 10-SEP-1998; 98US-0099808P.
XX PR 10-SEP-1998; 98US-0099812P.
XX PR 10-SEP-1998; 98US-0099815P.
XX PR 10-SEP-1998; 98US-0099816P.
XX PR 15-SEP-1998; 98US-0100388P.
XX PR 15-SEP-1998; 98US-0100390P.
XX PR 16-SEP-1998; 98US-0100584P.
XX PR 16-SEP-1998; 98US-0100627P.
XX PR 16-SEP-1998; 98US-0100661P.
XX PR 16-SEP-1998; 98US-0100662P.
XX PR 16-SEP-1998; 98US-0100664P.
XX PR 17-SEP-1998; 98US-0100683P.
XX PR 17-SEP-1998; 98US-0100684P.
XX PR 17-SEP-1998; 98US-0100710P.
XX PR 17-SEP-1998; 98US-0100711P.
XX PR 17-SEP-1998; 98US-0100913P.
XX PR 17-SEP-1998; 98US-0100919P.
XX PR 18-SEP-1998; 98US-0100848P.
XX PR 18-SEP-1998; 98US-0100849P.
XX PR 18-SEP-1998; 98US-0101014P.
XX PR 18-SEP-1998; 98US-0101068P.
XX PR 18-SEP-1998; 98US-0101071P.
XX PR 22-SEP-1998; 98US-0101279P.
XX PR 23-SEP-1998; 98US-0101471P.
XX PR 23-SEP-1998; 98US-0101472P.
XX PR 23-SEP-1998; 98US-0101474P.
XX PR 23-SEP-1998; 98US-0101475P.
XX PR 23-SEP-1998; 98US-0101476P.
XX PR 23-SEP-1998; 98US-0101477P.
XX PR 23-SEP-1998; 98US-0101479P.
XX PR 24-SEP-1998; 98US-0101738P.
XX PR 24-SEP-1998; 98US-0101741P.
XX PR 24-SEP-1998; 98US-0101743P.
XX PR 24-SEP-1998; 98US-0101915P.
XX PR 24-SEP-1998; 98US-0101916P.
XX PR 29-SEP-1998; 98US-0102207P.
XX PR 29-SEP-1998; 98US-0102207P.
XX PR 29-SEP-1998; 98US-0102240P.
XX PR 29-SEP-1998; 98US-0102307P.
XX PR 29-SEP-1998; 98US-0102330P.
XX PR 30-SEP-1998; 98US-0102331P.
XX PR 30-SEP-1998; 98US-0102484P.
XX PR 30-SEP-1998; 98US-0102487P.
XX PR 30-SEP-1998; 98US-0102570P.

PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103311P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106031P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 30-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106903P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 18-NOV-1998; 98US-0108904P.
PR (GETH) GENENTECH INC.
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX WPI; 2000-237871/20.
XX N-PSDB; AAA37075.
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
XX PRO polypeptides, useful for screening of potential peptide or small

PT molecule inhibitors of the relevant receptor/ligand interactions.
XX Claim 12; Fig 108; 773pp; English.
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention
XX Sequence 248 AA;
SQ
Query Match 100.0%; Score 1374; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTA 60
DB 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTA 60
QY 61 AHCSGSRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPV 120
DB 61 AHCSGSRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPV 120
QY 121 TSSVQPLPLPNDCATAGTECHVSCWGITNHPNPPFDLLQCLNLSIVSHATCHGVYPERI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSCWGITNHPNPPFDLLQCLNLSIVSHATCHGVYPERI 180
QY 181 TSNMVCAGGVPQDACCQDSGGPLVCGGVLOGLVSGVSGPCGQDGPVYTYICKYVDW 240
DB 181 TSNMVCAGGVPQDACCQDSGGPLVCGGVLOGLVSGVSGPCGQDGPVYTYICKYVDW 240
QY 241 IRIMLRNN 248
DB 241 IRIMLRNN 248
RESULT 5
AAM23994
ID AAM23994 standard; protein; 248 AA.
XX
AC AAM23994;
XX
DT 12-OCT-2001 (first entry)
XX Human EST encoded protein SEQ ID NO: 1519.
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX Homo sapiens.
XX WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI; 2001-476164/51.
DR N-PSDB; AAH98653.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
XX
XX Claim 20; Page 1048-1049; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
XX
SQ Sequence 248 AA;
Query Match 100.0%; Score 1374; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSIFLLLCVGLGSLQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWVLT 60
DB 1 MGLSIFLLLCVGLGSLQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWVLT 60
QY 61 AHCSGSRVYVRLGEHSLSQLDTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
DB 61 AHCSGSRVYVRLGEHSLSQLDTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPFDPDLQLCLNLSIVSHATCHGVYVPGRI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPFDPDLQLCLNLSIVSHATCHGVYVPGRI 180
QY 181 TSNMVCAGVPGQDACQDGGPLVCGVGLQGLVSGSVGPGCGDGIPIGVYTYICKYVDW 240
DB 181 TSNMVCAGVPGQDACQDGGPLVCGVGLQGLVSGSVGPGCGDGIPIGVYTYICKYVDW 240
QY 241 IRMIMRNN 248
DB 241 IRMIMRNN 248
RESULT 6
AAB66142
ID AAB66142 standard; protein; 248 AA.
XX
XX AAB66142;
AC
XX
DT 02-APR-2001 (first entry)
XX
DE Protein of the invention #54.
XX
XX Secreted; transmembrane; gene therapy.
XX
XX Unidentified.
XX
XX W0200078961-A1.
PN
XX
XX 28-DEC-2000.
PD
XX
XX 18-FEB-2000; 2000WO-US004342.
PF
XX
XX 23-JUN-1999; 99US-0141037P.
PR
XX 20-JUL-1999; 99US-0144758P.
PR
XX 26-JUL-1999; 99US-0145698P.
PR
XX 01-SEP-1999; 99WO-US020111.
PR
XX 29-OCT-1999; 99US-0162506P.
PR
XX 30-NOV-1999; 99WO-US028313.
PR
XX 02-DEC-1999; 99WO-US028551.
PR
XX 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
XX
XX Claim 1; Fig 108; 787pp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
XX
SQ Sequence 248 AA;
Query Match 100.0%; Score 1374; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSIFLLLCVGLGSLQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWVLT 60
DB 1 MGLSIFLLLCVGLGSLQAATPKIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWVLT 60
QY 61 AHCSGSRVYVRLGEHSLSQLDTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
DB 61 AHCSGSRVYVRLGEHSLSQLDTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPFDPDLQLCLNLSIVSHATCHGVYVPGRI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPFDPDLQLCLNLSIVSHATCHGVYVPGRI 180
QY 181 TSNMVCAGVPGQDACQDGGPLVCGVGLQGLVSGSVGPGCGDGIPIGVYTYICKYVDW 240
DB 181 TSNMVCAGVPGQDACQDGGPLVCGVGLQGLVSGSVGPGCGDGIPIGVYTYICKYVDW 240
QY 241 IRMIMRNN 248
DB 241 IRMIMRNN 248
RESULT 7
ABO33635
ID ABO33635 standard; protein; 248 AA.
XX
XX ABO33635;
AC
XX
XX 17-SEP-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO1303.
XX
XX Human; secreted and transmembrane protein; PRO; angiogenesis;
KW endothelial cell proliferation; wound healing; immune response;
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
KW cardiac insufficiency disorder; calcium flux; inflammation;
KW vascular endothelial growth factor-stimulated proliferation;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
KW pancreatic beta-cell precursor cell differentiation; thalassemias;
KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
KW

cartilage disorder; sports injury; arthritis.

KW
XX OS Homo sapiens.
XX PN US2003073130-A1.
XX PD 17-APR-2003.
XX PF 11-DEC-2001; 2001US-00015869.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
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 PA (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2003-585293/55.
 DR N-PSDB; ACD68378.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
 PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
 PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

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 Best Local Similarity 100.0%; Pred. No. 3.8e-98;
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 AC ABO44488;
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 DT 01-OCT-2003 (first entry)
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KW antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
 KW adrenal cortical capillary; endothelial cell growth; wound healing;
 KW stimulated T-lymphocyte proliferation; immune response suppression;
 KW neonatal heart hypertrophy; cardiac insufficiency disorder;
 KW vascular endothelial growth factor; inflammation; mononuclear cell;
 KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
 KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
 KW sports injury; arthritis.
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 OS Homo sapiens.
 XX US2003044841-A1.
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XX (GETH ) GENENTECH INC.
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XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams PM, Wood WI;
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XX WPI: 2003-492259/46.
DR N-PSDB; ACH04480.
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XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating various cardiac insufficiency
PT disorders, bone and/or cartilage disorders such as sports injuries and
PT arthritis.

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XX DT
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KW tissue typing; chromosome identification; vaccine.
XX Homo sapiens.
XX US2003073129-A1.
XX 17-APR-2003.
XX 04-SEP-2001; 2001US-00946374.
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PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0108464P.
PR 30-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.

PR 12-APR-1999; 99US-00284291.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 18-OCT-1999; 99US-00403297.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-0082636.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX XX

(GETH) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood MT;
XX WPI: 2003-585292/55.
DR N-PSDB; ACD68024.

XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX Claim 12; Fig 108; 561pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (1), having at least 80% sequence identity to a sequence

Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTA 60
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QY 61 AHCSGRYWRVRLGHELSQLDWTQTRHSGFVTHPGYLGASTSHEHDLRLRLPVRV 120
DB 61 AHCSGRYWRVRLGHELSQLDWTQTRHSGFVTHPGYLGASTSHEHDLRLRLPVRV 120
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGTINHPRPFPDQLQCLNLSVSHATCHGVYPGRI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGTINHPRPFPDQLQCLNLSVSHATCHGVYPGRI 180
QY 181 TSNMVCAGGVPQDACCQDSGGPLVCGGVLQGLVSMGSGVPCQDGIPIGVYVICKYVDW 240
DB 181 TSNMVCAGGVPQDACCQDSGGPLVCGGVLQGLVSMGSGVPCQDGIPIGVYVICKYVDW 240

Db 181 TSNMVCAGGVPQDACCQDSGGPLVCGGVLQGLVSMGSGVPCQDGIPIGVYVICKYVDW 240
QY 241 IRMIMRNN 248
DB 241 IRMIMRNN 248
RESULT 10
ADCL18063
ID ADC18063 standard; protein; 248 AA.
XX AC ADC18063;
XX 18-DEC-2003 (first entry)
XX Human PRO polypeptide #54.
XX Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;
XX genetic disorder.
XX Homo sapiens.
XX US2003064925-A1.
XX 03-APR-2003.
XX 10-DEC-2001; 2001US-00013907.
XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
XX 09-SEP-1998; 98US-0099536P.
XX 09-SEP-1998; 98US-0099596P.
XX 09-SEP-1998; 98US-0099598P.
XX 09-SEP-1998; 98US-0099602P.
XX 09-SEP-1998; 98US-0099642P.
XX 10-SEP-1998; 98US-0099741P.
XX 10-SEP-1998; 98US-0099754P.
XX 10-SEP-1998; 98US-0099763P.
XX 10-SEP-1998; 98US-0099792P.
XX 10-SEP-1998; 98US-0099808P.
XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98US-0099815P.
XX 10-SEP-1998; 98US-0099816P.
XX 15-SEP-1998; 98US-0100385P.
XX 15-SEP-1998; 98US-0100388P.
XX 15-SEP-1998; 98US-0100390P.
XX 16-SEP-1998; 98US-0100584P.
XX 16-SEP-1998; 98US-0100627P.
XX 16-SEP-1998; 98US-0100661P.
XX 16-SEP-1998; 98US-0100662P.
XX 16-SEP-1998; 98US-0100664P.
XX 17-SEP-1998; 98US-0100683P.
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XX 17-SEP-1998; 98US-0100919P.
XX 17-SEP-1998; 98US-0100930P.
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XX 18-SEP-1998; 98US-0100849P.
XX 18-SEP-1998; 98US-0101014P.
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XX 23-SEP-1998; 98US-0101471P.
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XX 23-SEP-1998; 98US-0101475P.
XX 23-SEP-1998; 98US-0101476P.

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PR	24-SEP-1998;	98US-0101743P.	PR	18-NOV-1998;	98US-0108904P.
PR	24-SEP-1998;	98US-0101915P.	PR	22-DEC-1998;	98US-0113296P.
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PR	29-SEP-1998;	98US-0102207P.	PR	05-JAN-1999;	99WO-US000106.
PR	29-SEP-1998;	98US-0102240P.	PR	16-APR-1999;	99US-0129674P.
PR	29-SEP-1998;	98US-0102307P.	PR	23-JUN-1999;	99US-0141037P.
PR	29-SEP-1998;	98US-0102330P.	PR	26-JUL-1999;	99US-0144758P.
PR	29-SEP-1998;	98US-0102331P.	PR	26-JUL-1999;	99US-0145698P.
PR	30-SEP-1998;	98US-0102484P.	PR	01-SEP-1999;	99WO-US020111.
PR	30-SEP-1998;	98US-0102487P.	PR	15-SEP-1999;	99WO-US021194.
PR	30-SEP-1998;	98US-0102570P.	PR	29-OCT-1999;	98US-0162506P.
PR	30-SEP-1998;	98US-0102571P.	PR	30-NOV-1999;	99WO-US028313.
PR	01-OCT-1998;	98US-0102684P.	PR	02-DEC-1999;	99WO-US028551.
PR	01-OCT-1998;	98US-0102687P.	PR	16-DEC-1999;	99WO-US030095.
PR	02-OCT-1998;	98US-0102965P.	PR	05-JAN-2000;	2000WO-US000219.
PR	06-OCT-1998;	98US-0103258P.	PR	06-JAN-2000;	2000WO-US000376.
PR	08-OCT-1998;	98US-0103449P.	PR	11-FEB-2000;	2000WO-US003565.
PR	07-OCT-1998;	98US-0103314P.	PR	18-FEB-2000;	2000WO-US004342.
PR	07-OCT-1998;	98US-0103315P.	PR	24-FEB-2000;	2000WO-US005004.
PR	07-OCT-1998;	98US-0103328P.	PR	03-MAR-2000;	2000WO-US005841.
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PR	07-OCT-1998;	98US-0103396P.	PR	17-MAY-2000;	2000WO-US013705.
PR	07-OCT-1998;	98US-0103401P.	PR	22-MAY-2000;	2000WO-US014042.
PR	08-OCT-1998;	98US-0103633P.	PR	30-MAY-2000;	2000WO-US014941.
PR	08-OCT-1998;	98US-0103678P.	PR	02-JUN-2000;	2000WO-US015264.
PR	08-OCT-1998;	98US-0103799P.	PR	23-AUG-2000;	2000WO-US023522.
PR	08-OCT-1998;	98US-0103711P.	PR	24-AUG-2000;	2000WO-US023328.
PR	14-OCT-1998;	98US-0104257P.	PR	08-NOV-2000;	2000WO-US030952.
PR	20-OCT-1998;	98US-0104987P.	PR	10-NOV-2000;	2000WO-US030873.
PR	20-OCT-1998;	98US-0105000P.	PR	01-DEC-2000;	2000WO-US032678.
PR	20-OCT-1998;	98US-0105002P.	PR	28-FEB-2001;	2001WO-US006520.
PR	21-OCT-1998;	98US-0105104P.	PR	01-MAR-2001;	2001WO-US005666.
PR	22-OCT-1998;	98US-0105169P.	PR	20-JUN-2001;	2001WO-US017800.
PR	22-OCT-1998;	98US-0105266P.	PR	20-JUN-2001;	2001WO-US019692.
PR	26-OCT-1998;	98US-0105693P.	PR	29-JUN-2001;	2001WO-US021066.
PR	26-OCT-1998;	98US-0105694P.	PR	09-JUL-2001;	2001WO-US021735.
PR	27-OCT-1998;	98US-0105807P.	PR	04-SEP-2001;	2001US-00946374.
PR	27-OCT-1998;	98US-0105881P.	XX		
PR	27-OCT-1998;	98US-0105882P.	PA	(GETH) GENENTECH INC.	
PR	28-OCT-1998;	98US-0106062P.	XX	Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;	
PR	28-OCT-1998;	98US-0106023P.	PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;	
PR	28-OCT-1998;	98US-0106029P.	PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;	
PR	28-OCT-1998;	98US-0106030P.	PI	Williams PM, Wood WI;	
PR	28-OCT-1998;	98US-0106032P.	XX	WPI; 2003-555602/52.	
PR	28-OCT-1998;	98US-0106033P.	DR	N-FSDP; ADC18062.	
PR	28-OCT-1998;	98US-0106248P.	DR		
PR	29-OCT-1998;	98US-0106384P.	XX	Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the	
PR	29-OCT-1998;	98US-0108500P.	PT	preparation of a medicament for treating a condition responsive to PRO	
PR	30-OCT-1998;	98US-0106464P.	PT	polypeptide, and as therapeutic agents e.g. vaccines.	
PR	03-NOV-1998;	98US-0106856P.	XX		
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PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 24-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US015264.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 01-DEC-2000; 2000WO-US032678.
PR 01-DEC-2000; 2000WO-US032678.
PR 01-MAR-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001WO-US046374.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI: 2003-874602/81.
DR N-PSDB; ADD70708.
XX
XX Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
XX
XX Claim 12; SEQ ID NO 194; 553pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC
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Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPVQVGLFEGTSLRCGGVLIDHRWVLT 60
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Db 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPVQVGLFEGTSLRCGGVLIDHRWVLT 60
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QY 61 AHCSSGRYVRLGEHLSQLDWTQIRHSGFVTHPGYLGASTSHEHDLRLRLRPVRV 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 AHCSSGRYVRLGEHLSQLDWTQIRHSGFVTHPGYLGASTSHEHDLRLRLRPVRV 120
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QY 121 TSSVQPLPLFNDCATAGTECHVSGWGITNHRNPFDPDLQLCLNLSIVSHATCHGVYPGRI 180
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Db 121 TSSVQPLPLFNDCATAGTECHVSGWGITNHRNPFDPDLQLCLNLSIVSHATCHGVYPGRI 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 181 TSNMVCAGGVPGQDACQDGGGLVCGGVLCGLVSGSVGPGCGDGIPIGVYTI CKYVDW 240
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Db 181 TSNMVCAGGVPGQDACQDGGGLVCGGVLCGLVSGSVGPGCGDGIPIGVYTI CKYVDW 240
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QY 241 IRMIMRNN 248
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 12
ADD39786
ID ADD39786 standard; protein; 248 AA.
XX
XX AC ADD39786;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human secreted/transmembrane protein PRO1303.
XX
XX Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
XX Homo sapiens.
XX
XX OS US2003083462-A1.
XX
XX 01-MAY-2003.
XX
XX 10-DEC-2001; 2001US-00013913.
XX
XX 05-JAN-1999; 99WO-US000106.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021194.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 16-DEC-1999; 99WO-US030095.
XX 06-JAN-2000; 2000WO-US000219.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004342.
XX 24-FEB-2000; 2000WO-US005841.
XX 02-MAR-2000; 2000WO-US006884.
XX 15-MAR-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 24-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US015264.
XX 02-JUN-2000; 2000WO-US015264.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 10-NOV-2000; 2000WO-US030952.
XX 01-DEC-2000; 2000WO-US032678.
XX 01-DEC-2000; 2000WO-US032678.
XX 01-DEC-2000; 2000WO-US032678.
XX 01-MAR-2001; 2001WO-US006520.
XX 01-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-JUL-2001; 2001WO-US021735.
XX 04-SEP-2001; 2001WO-US046374.
XX
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PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-755122/71.
DR N-PSDB; ADD39785.
XX
XX New secreted and transmembrane PRO polypeptides useful for treating
PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
PT hypo-insulinemia, sports injuries and arthritis.
XX
XX Claim 12; SEQ ID NO 194; 557pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides). Also include are the
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimeric molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. Pro is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful in generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
CC polypeptides are useful for suppressing immune response. PRO1246
CC polypeptide is useful for treating cardiac insufficiency disorders.
CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
CC PRO1561 polypeptide are useful for stimulating calcium flux in human
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC polypeptides are useful for treating bone and/or cartilage disorders
CC (e.g., arthritis) and wound healing. PRO130, PRO1275 and PRO1418
CC polypeptides are useful for treating diabetes in skeletal muscle cells
CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC treating Berger disease or other nephropathies associated with Schonlein-
CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
CC sequence represents a PRO protein of the invention.
XX
XX Sequence 248 AA;
SQ
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
DB 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
QY 61 AHCSGSRVWRLGHEHSLSQLDWTQEIHSFGSVTHPGVLGASTSHEHDLRLRLPVRV 120
DB 61 AHCSGSRVWRLGHEHSLSQLDWTQEIHSFGSVTHPGVLGASTSHEHDLRLRLPVRV 120
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGTNHNPPNPPDLQCLNLSIVSHATCHGVYPCRI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGTNHNPPNPPDLQCLNLSIVSHATCHGVYPCRI 180
QY 181 TSNMVCAGGVFGQDACQDSDGSLVCGGVLQSLVSGVSGPGQDGFEGVVTYICKYVDW 240

DB 181 TSNMVCAGGVFGQDACQDSDGSLVCGGVLQSLVSGVSGPGQDGFEGVVTYICKYVDW 240
QY 241 IRMIMRNN 248
DB 241 IRMIMRNN 248
RESULT 13
ADD70232
ID ADD70232 standard; protein; 248 AA.
XX
AC ADD70232;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane protein PRO1303.
XX
KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
XX US2003054406-A1.
PD 20-MAR-2003.
XX
PF 06-DEC-2001; 2001US-00006818.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 02-SEP-1998; 98US-0098936P.
PR 03-SEP-1998; 98US-0098956P.
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PR 03-SEP-1998; 98US-0098960P.
PR 09-SEP-1998; 98US-0098964P.
PR 09-SEP-1998; 98US-0098974P.
PR 10-SEP-1998; 98US-00989754P.
PR 10-SEP-1998; 98US-00989763P.
PR 10-SEP-1998; 98US-00989792P.
PR 10-SEP-1998; 98US-00989808P.
PR 10-SEP-1998; 98US-00989812P.
PR 10-SEP-1998; 98US-00989815P.
PR 10-SEP-1998; 98US-00989816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
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PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
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PR 22-SEP-1998; 98US-0101279P.
PR

PR 23-SEP-1998; 98US-0101471P.
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PR 23-SEP-1998; 98US-0101477P.
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PR 24-SEP-1998; 98US-0101738P.
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PR 24-SEP-1998; 98US-0101916P.
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PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
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PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
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PR 14-OCT-1998; 98US-0104257P.
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PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
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PR 27-OCT-1998; 98US-0105807P.
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PR 28-OCT-1998; 98US-0106023P.
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PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
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PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.

PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
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PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 98US-0114223P.
PR 16-APR-1999; 98US-0129674P.
PR 23-JUN-1999; 98US-0141037P.
PR 20-JUL-1999; 98US-0144758P.
PR 26-JUL-1999; 98US-0145698P.
PR 01-SEP-1999; 98US-0145698P.
PR 15-SEP-1999; 98US-0145698P.
PR 29-SEP-1999; 98US-0145698P.
PR 30-NOV-1999; 98US-0145698P.
PR 02-DEC-1999; 98US-0145698P.
PR 16-DEC-1999; 98US-0145698P.
PR 05-JAN-2000; 98US-0145698P.
PR 06-JAN-2000; 98US-0145698P.
PR 11-FEB-2000; 98US-0145698P.
PR 18-FEB-2000; 98US-0145698P.
PR 24-FEB-2000; 98US-0145698P.
PR 02-MAR-2000; 98US-0145698P.
PR 15-MAR-2000; 98US-0145698P.
PR 17-MAY-2000; 98US-0145698P.
PR 22-MAY-2000; 98US-0145698P.
PR 30-MAY-2000; 98US-0145698P.
PR 02-JUN-2000; 98US-0145698P.
PR 23-AUG-2000; 98US-0145698P.
PR 24-AUG-2000; 98US-0145698P.
PR 08-NOV-2000; 98US-0145698P.
PR 10-NOV-2000; 98US-0145698P.
PR 01-DEC-2000; 98US-0145698P.
PR 28-FEB-2001; 98US-0145698P.
PR 01-MAR-2001; 98US-0145698P.
PR 20-JUN-2001; 98US-0145698P.
PR 29-JUN-2001; 98US-0145698P.
PR 09-JUL-2001; 98US-0145698P.
PR 04-SEP-2001; 98US-0145698P.

(GETH) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;

WPI; 2003-708344/67.
N-PSDB; ADD70231.

Novel isolated PRO polypeptide useful for tissue typing, modulating
biological activity of cell, as molecular weight markers in protein
electrophoresis, for treating arthritis, tumor.

Claim 12; SEQ ID NO 194; 549pp; English.

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 1374; DB 7; Length 248;

Best Local Similarity 100.0%; Pred. No. 3.8e-98;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVLGLSQAATPKIFNGTCGRNSQPWQVGLFGTSLRCGVLIDHRWLTA 60

DB 1 MGLSIFLLLCVLGLSQAATPKIFNGTCGRNSQPWQVGLFGTSLRCGVLIDHRWLTA 60

Qy 61 AHCSGRYVRLGHSLSQLDWTEQIRHSGFVTHPCYLGASTSHEHDLRLRLPVRV 120
 Db 61 AHCSGRYVRLGHSLSQLDWTEQIRHSGFVTHPCYLGASTSHEHDLRLRLPVRV 120
 Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGTINHPNPFDDLLQCLNLSIVSHATCHGVYFGR 180
 Db 121 TSSVQPLPLPNDCATAGTECHVSGWGTINHPNPFDDLLQCLNLSIVSHATCHGVYFGR 180
 Qy 181 TSNMVCAGGVPQDACQDGGPLVCGGVLOGLVSGVSGVPCGGDGPVGVYTI CKYVDW 240
 Db 181 TSNMVCAGGVPQDACQDGGPLVCGGVLOGLVSGVSGVPCGGDGPVGVYTI CKYVDW 240
 Qy 241 IRMIMRN 248
 Db 241 IRMIMRN 248

RESULT 14

ADD38353
 ID ADD38353 standard; protein; 248 AA.
 AC ADD38353;
 DT 15-JAN-2004 (first entry)
 DE Human secreted/transmembrane protein PRO1303.
 KW Human; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.
 OS Homo sapiens.
 XX US2003096955-A1.
 PN 22-MAY-2003.
 PD 07-DEC-2001; 2001US-00012755.
 PF 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
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 PR 09-SEP-1998; 98US-0099536P.
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 PR 10-SEP-1998; 98US-0099792P.
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PR 17-SEP-1998; 98US-0100711P.
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 PR 18-SEP-1998; 98US-0100849P.
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 PR 08-OCT-1998; 98US-0103633P.
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 PR 22-OCT-1998; 98US-0105169P.
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PR	10-NOV-1998;	98US-0107783P.	Query Match	100.0%;	Score 1374;	DB 7;	Length 248;
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PR	17-NOV-1998;	98US-0108806P.					
PR	17-NOV-1998;	98US-0108807P.					
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PR	18-NOV-1998;	98US-0108904P.					
PR	22-DEC-1998;	98US-0113296P.					
PR	30-DEC-1998;	98US-0114223P.					
PR	05-JAN-1999;	99WO-US000106.					
PR	16-APR-1999;	99US-0129674P.					
PR	23-JUN-1999;	99US-0141037P.					
PR	20-JUL-1999;	99US-0144758P.					
PR	26-JUL-1999;	99US-0145698P.					
PR	01-SEP-1999;	99WO-US020111.					
PR	15-SEP-1999;	99WO-US021194.					
PR	29-OCT-1999;	99US-0162506P.					
PR	30-NOV-1999;	99WO-US028313.					
PR	02-DEC-1999;	99WO-US028551.					
PR	16-DEC-1999;	99WO-US030059.					
PR	05-JAN-2000;	2000WO-US000219.					
PR	06-JAN-2000;	2000WO-US000376.					
PR	11-FEB-2000;	2000WO-US003565.					
PR	18-FEB-2000;	2000WO-US004342.					
PR	24-FEB-2000;	2000WO-US005004.					
PR	02-MAR-2000;	2000WO-US005841.					
PR	15-MAR-2000;	2000WO-US006884.					
PR	17-MAY-2000;	2000WO-US013705.					
PR	22-MAY-2000;	2000WO-US014042.					
PR	30-MAY-2000;	2000WO-US014941.					
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PR	23-AUG-2000;	2000WO-US023522.					
PR	24-AUG-2000;	2000WO-US023328.					
PR	08-NOV-2000;	2000WO-US030952.					
PR	10-NOV-2000;	2000WO-US030873.					
PR	01-DEC-2000;	2000WO-US032678.					
PR	28-FEB-2001;	2001WO-US000520.					
PR	01-MAR-2001;	2001WO-US000666.					
PR	01-JUN-2001;	2001WO-US017800.					
PR	20-JUN-2001;	2001WO-US019692.					
PR	29-JUN-2001;	2001WO-US021066.					
PR	09-JUL-2001;	2001WO-US021735.					
PR	04-SEP-2001;	2001US-00946374.					
XX							
PA	(GETH) GENENTECH INC.						
XX							
PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;						
PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;						
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;						
PI	Williams PM, Wood WI;						
XX							
DR	WPI; 2003-787000/74.						
DR	N-PSDB; ADD38352.						
XX							
XX							
PT	Novel isolated PRO polypeptide, useful for treating cancerous tumors,						
PT	cardiac insufficiency disorders, wound healing, diabetes mellitus,						
PT	thalassemias.						
XX							
PS	Claim 12; SEQ ID NO 194; 556pp; English.						
XX							
CC	The invention relates to an isolated PRO polypeptide (secreted or						
CC	transmembrane protein) having at least 80% amino acid sequence identity						

Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S; Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan Ku; Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK; Williams PM, Wood WI; WPI: 2003-786999/74.

DR N-PSDB; ADD39308.
XX Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
PS Claim 12; SEQ ID NO 194; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSIFLLLCVGLSQATPKIFNGTEGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
DB 1 MGLSIFLLLCVGLSQATPKIFNGTEGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
QY 61 AHCSGSRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
DB 61 AHCSGSRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGIITNHPNPPDILQCLNLSIVSHATCHGVYPGRI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGIITNHPNPPDILQCLNLSIVSHATCHGVYPGRI 180
QY 181 TSNMVCAGGVPQDACQDGGPLVCGGVLSWGSVPGCGQDGIPIGVVYTYICKYVDW 240
DB 181 TSNMVCAGGVPQDACQDGGPLVCGGVLSWGSVPGCGQDGIPIGVVYTYICKYVDW 240
QY 241 IRMIMRNN 248
DB 241 IRMIMRNN 248

Search completed: June 15, 2004, 16:15:08
Job time : 62 secs